

SEQUENCE LISTING

<110> BIOCHEM PHARMA INC.
 HAMEL, Josée
 BRODEUR, Bernard R.
 PINEAU, Isabelle
 MARTIN, Denis
 RIOUX, Clément

<120> NOVEL STREPTOCOCCUS ANTIGENS

<130> 12806-11PCT

<150> US 60/113,800

<151> 1998-12-23

<160> 102

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 3120

<212> DNA

<213> S. pneumoniae

<220>

<400> 1

atg	aaa	ttt	agt	aaa	aaa	tat	ata	gca	gct	gga	tca	gct	gtt	atc	gta	48
tcc	ttg	agt	cta	tgt	gcc	tat	gca	cta	aac	cag	cat	cgt	tcg	cag	gaa	96
aat	aag	gac	aat	aat	cgt	gtc	tct	tat	gtg	gat	ggc	agc	cag	tca	agt	144
cag	aaa	agt	gaa	aac	ttg	aca	cca	gac	cag	gtt	agc	cag	aaa	gaa	gga	192
att	cag	gct	gag	caa	att	gta	atc	aaa	att	aca	gat	cag	ggc	tat	gta	240
acg	tca	cac	ggt	gac	cac	tat	cat	tac	tat	aat	ggg	aaa	gtt	cct	tat	288
gat	gcc	ctc	ttt	agt	gaa	gaa	ctc	ttg	atg	aag	gat	cca	aac	tat	caa	336
ctt	aaa	gac	gct	gat	att	gtc	aat	gaa	gtc	aag	ggt	ggt	tat	atc	atc	384
aag	gtc	gat	gga	aaa	tat	tat	gtc	tac	ctg	aaa	gat	gca	gct	cat	gct	432
gat	aat	gtt	cga	act	aaa	gat	gaa	atc	aat	cgt	caa	aaa	caa	gaa	cat	480
gtc	aaa	gat	aat	gag	aag	gtt	aac	tct	aat	gtt	gct	gta	gca	agg	tct	528
cag	gga	cga	tat	acg	aca	aat	gat	ggt	tat	gtc	ttt	aat	cca	gct	gat	576
att	atc	gaa	gat	acg	ggt	aat	gct	tat	atc	gtt	cct	cat	gga	ggt	cac	624
tat	cac	tac	att	ccc	aaa	agc	gat	tta	tct	gct	agt	gaa	tta	gca	gca	672
gct	aaa	gca	cat	ctg	gct	gga	aaa	aat	atg	caa	ccg	agt	cag	tta	agc	720
tat	tct	tca	aca	gct	agt	gac	aat	aac	acg	caa	tct	gta	gca	aaa	gga	768
tca	act	agc	aag	cca	gca	aat	aaa	tct	gaa	aat	ctc	cag	agt	ctt	ttg	816
aag	gaa	ctc	tat	gat	tca	cct	agc	gcc	caa	cgt	tac	agt	gaa	tca	gat	864
ggc	ctg	gtc	ttt	gac	cct	gct	aag	att	atc	agt	cgt	aca	cca	aat	gga	912
gtt	gcg	att	ccg	cat	ggc	gac	cat	tac	cac	ttt	att	cct	tac	agc	aag	960
ctt	tct	gct	tta	gaa	gaa	aag	att	gcc	aga	atg	gtg	cct	atc	agt	gga	1008
act	ggt	tct	aca	gtt	tct	aca	aat	gca	aaa	cct	aat	gaa	gta	gtg	tct	1056
agt	cta	ggc	agt	ctt	tca	agc	aat	cct	tct	tct	tta	acg	aca	agt	aag	1104
gag	ctc	tct	tca	gca	tct	gat	ggt	tat	att	ttt	aat	cca	aaa	gat	atc	1152
gtt	gaa	gaa	acg	gct	aca	gct	tat	att	gta	aga	cat	ggt	gat	cat	ttc	1200
cat	tac	att	cca	aaa	tca	aat	caa	att	ggg	caa	ccg	act	ctt	cca	aac	1248



```

aat agt cta gca aca cct tct cca tct ctt cca atc aat cca gga act 1296
tca cat gag aaa cat gaa gaa gat gga tac gga ttt gat gct aat cgt 1344
att atc gct gaa gat gaa tca ggt ttt gtc atg agt cac gga gac cac 1392
aat cat tat ttc ttc aag aag gac ttg aca gaa gag caa att aag gct 1440
gcg caa aaa cat tta gag gaa gtt aaa act agt cat aat gga tta gat 1488
tct ttg tca tct cat gaa cag gat tat cca ggt aat gcc aaa gaa atg 1536
aaa gat tta gat aaa aaa atc gaa gaa aaa att gct ggc att atg aaa 1584
caa tat ggt gtc aaa cgt gaa agt att gtc gtg aat aaa gaa aaa aat 1632
gcg att att tat ccg cat gga gat cac cat cat gca gat ccg att gat 1680
gaa cat aaa ccg gtt gga att ggt cat tct cac agt aac tat gaa ctg 1728
ttt aaa ccc gaa gaa gga gtt gct aaa aaa gaa ggg aat aaa gtt tat 1776
act gga gaa gaa tta acg aat gtt gtt aat ttg tta aaa aat agt acg 1824
ttt aat aat caa aac ttt act cta gcc aat ggt caa aaa cgc gtt tct 1872
ttt agt ttt ccg cct gaa ttg gag aaa aaa tta ggt atc aat atg cta 1920
gta aaa tta ata aca cca gat gga aaa gta ttg gag aaa gta tct ggt 1968
aaa gta ttt gga gaa gga gta ggg aat att gca aac ttt gaa tta gat 2016
caa cct tat tta cca gga caa aca ttt aag tat act atc gct tca aaa 2064
gat tat cca gaa gta agt tat gat ggt aca ttt aca gtt cca acc tct 2112
tta gct tac aaa atg gcc agt caa acg att ttc tat cct ttc cat gca 2160
ggg gat act tat tta aga gtg aac cct caa ttt gca gtg cct aaa gga 2208
act gat gct tta gtc aga gtg ttt gat gaa ttt cat gga aat gct tat 2256
tta gaa aat aac tat aaa gtt ggt gaa atc aaa tta ccg att ccg aaa 2304
tta aac caa gga aca acc aga acg gcc gga aat aaa att cct gta acc 2352
ttc atg gca aat gct tat ttg gac aat caa tgc act tat att gtg gaa 2400
gta cct atc ttg gaa aaa gaa aat caa act gat aaa cca agt att cta 2448
cca caa ttt aaa agg aat aaa gca caa gaa aac tca aaa ctt gat gaa 2496
aag gta gaa gaa cca aag act agt gag aag gta gaa aaa gaa aaa ctt 2544
tct gaa act ggg aat agt act agt aat tca acg tta gaa gaa gtt cct 2592
aca gtg gat cct gta caa gaa aaa gta gca aaa ttt gct gaa agt tat 2640
ggg atg aag cta gaa aat gtc ttg ttt aat atg gac gga aca att gaa 2688
tta tat tta cca tca gga gaa gtc att aaa aag aat atg gca gat ttt 2736
aca gga gaa gca cct caa gga aat ggt gaa aat aaa cca tct gaa aat 2784
gga aaa gta tct act gga aca gtt gag aac caa cca aca gaa aat aaa 2832
cca gca gat tct tta cca gag gca cca aac gaa aaa cct gta aaa cca 2880
gaa aac tca acg gat aat gga atg ttg aat cca gaa ggg aat gtg ggg 2928
agt gac cct atg tta gat cca gca tta gag gaa gct cca gca gta gat 2976
cct gta caa gaa aaa tta gaa aaa ttt aca gct agt tac gga tta ggc 3024
tta gat agt gtt ata ttc aat atg gat gga acg att gaa tta aga ttg 3072
cca agt gga gaa gtg ata aaa aag aat tta tct gat ttc ata gcg 3117
taa 3120

```

<210> 2

<211> 1039

<212> PRT

<213> S. pneumoniae

<400> 2

```

Met Lys Phe Ser Lys Lys Tyr Ile Ala Ala Gly Ser Ala Val Ile Val
 1          5          10          15
Ser Leu Ser Leu Cys Ala Tyr Ala Leu Asn Gln His Arg Ser Gln Glu
 20          25          30
Asn Lys Asp Asn Asn Arg Val Ser Tyr Val Asp Gly Ser Gln Ser Ser
 35          40          45
Gln Lys Ser Glu Asn Leu Thr Pro Asp Gln Val Ser Gln Lys Glu Gly
 50          55          60
Ile Gln Ala Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val
65          70          75          80

```

Thr Ser His Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr
 85 90 95
 Asp Ala Leu Phe Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln
 100 105 110
 Leu Lys Asp Ala Asp Ile Val Asn Glu Val Lys Gly Gly Tyr Ile Ile
 115 120 125
 Lys Val Asp Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala
 130 135 140
 Asp Asn Val Arg Thr Lys Asp Glu Ile Asn Arg Gln Lys Gln Glu His
 145 150 155 160
 Val Lys Asp Asn Glu Lys Val Asn Ser Asn Val Ala Val Ala Arg Ser
 165 170 175
 Gln Gly Arg Tyr Thr Thr Asn Asp Gly Tyr Val Phe Asn Pro Ala Asp
 180 185 190
 Ile Ile Glu Asp Thr Gly Asn Ala Tyr Ile Val Pro His Gly Gly His
 195 200 205
 Tyr His Tyr Ile Pro Lys Ser Asp Leu Ser Ala Ser Glu Leu Ala Ala
 210 215 220
 Ala Lys Ala His Leu Ala Gly Lys Asn Met Gln Pro Ser Gln Leu Ser
 225 230 235 240
 Tyr Ser Ser Thr Ala Ser Asp Asn Asn Thr Gln Ser Val Ala Lys Gly
 245 250 255
 Ser Thr Ser Lys Pro Ala Asn Lys Ser Glu Asn Leu Gln Ser Leu Leu
 260 265 270
 Lys Glu Leu Tyr Asp Ser Pro Ser Ala Gln Arg Tyr Ser Glu Ser Asp
 275 280 285
 Gly Leu Val Phe Asp Pro Ala Lys Ile Ile Ser Arg Thr Pro Asn Gly
 290 295 300
 Val Ala Ile Pro His Gly Asp His Tyr His Phe Ile Pro Tyr Ser Lys
 305 310 315 320
 Leu Ser Ala Leu Glu Glu Lys Ile Ala Arg Met Val Pro Ile Ser Gly
 325 330 335
 Thr Gly Ser Thr Val Ser Thr Asn Ala Lys Pro Asn Glu Val Val Ser
 340 345 350
 Ser Leu Gly Ser Leu Ser Ser Asn Pro Ser Ser Leu Thr Thr Ser Lys
 355 360 365
 Glu Leu Ser Ser Ala Ser Asp Gly Tyr Ile Phe Asn Pro Lys Asp Ile
 370 375 380
 Val Glu Glu Thr Ala Thr Ala Tyr Ile Val Arg His Gly Asp His Phe
 385 390 395 400
 His Tyr Ile Pro Lys Ser Asn Gln Ile Gly Gln Pro Thr Leu Pro Asn
 405 410 415
 Asn Ser Leu Ala Thr Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr
 420 425 430
 Ser His Glu Lys His Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg
 435 440 445
 Ile Ile Ala Glu Asp Glu Ser Gly Phe Val Met Ser His Gly Asp His
 450 455 460
 Asn His Tyr Phe Phe Lys Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala
 465 470 475 480
 Ala Gln Lys His Leu Glu Glu Val Lys Thr Ser His Asn Gly Leu Asp
 485 490 495
 Ser Leu Ser Ser His Glu Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met
 500 505 510
 Lys Asp Leu Asp Lys Lys Ile Glu Glu Lys Ile Ala Gly Ile Met Lys
 515 520 525

Gln Tyr Gly Val Lys Arg Glu Ser Ile Val Val Asn Lys Glu Lys Asn
 530 535 540
 Ala Ile Ile Tyr Pro His Gly Asp His His His Ala Asp Pro Ile Asp
 545 550 555 560
 Glu His Lys Pro Val Gly Ile Gly His Ser His Ser Asn Tyr Glu Leu
 565 570 575
 Phe Lys Pro Glu Glu Gly Val Ala Lys Lys Glu Gly Asn Lys Val Tyr
 580 585 590
 Thr Gly Glu Glu Leu Thr Asn Val Val Asn Leu Leu Lys Asn Ser Thr
 595 600 605
 Phe Asn Asn Gln Asn Phe Thr Leu Ala Asn Gly Gln Lys Arg Val Ser
 610 615 620
 Phe Ser Phe Pro Pro Glu Leu Glu Lys Lys Leu Gly Ile Asn Met Leu
 625 630 635 640
 Val Lys Leu Ile Thr Pro Asp Gly Lys Val Leu Glu Lys Val Ser Gly
 645 650 655
 Lys Val Phe Gly Glu Gly Val Gly Asn Ile Ala Asn Phe Glu Leu Asp
 660 665 670
 Gln Pro Tyr Leu Pro Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys
 675 680 685
 Asp Tyr Pro Glu Val Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser
 690 695 700
 Leu Ala Tyr Lys Met Ala Ser Gln Thr Ile Phe Tyr Pro Phe His Ala
 705 710 715 720
 Gly Asp Thr Tyr Leu Arg Val Asn Pro Gln Phe Ala Val Pro Lys Gly
 725 730 735
 Thr Asp Ala Leu Val Arg Val Phe Asp Glu Phe His Gly Asn Ala Tyr
 740 745 750
 Leu Glu Asn Asn Tyr Lys Val Gly Glu Ile Lys Leu Pro Ile Pro Lys
 755 760 765
 Leu Asn Gln Gly Thr Thr Arg Thr Ala Gly Asn Lys Ile Pro Val Thr
 770 775 780
 Phe Met Ala Asn Ala Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu
 785 790 795 800
 Val Pro Ile Leu Glu Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu
 805 810 815
 Pro Gln Phe Lys Arg Asn Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu
 820 825 830
 Lys Val Glu Glu Pro Lys Thr Ser Glu Lys Val Glu Lys Glu Lys Leu
 835 840 845
 Ser Glu Thr Gly Asn Ser Thr Ser Asn Ser Thr Leu Glu Glu Val Pro
 850 855 860
 Thr Val Asp Pro Val Gln Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr
 865 870 875 880
 Gly Met Lys Leu Glu Asn Val Leu Phe Asn Met Asp Gly Thr Ile Glu
 885 890 895
 Leu Tyr Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Met Ala Asp Phe
 900 905 910
 Thr Gly Glu Ala Pro Gln Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn
 915 920 925
 Gly Lys Val Ser Thr Gly Thr Val Glu Asn Gln Pro Thr Glu Asn Lys
 930 935 940
 Pro Ala Asp Ser Leu Pro Glu Ala Pro Asn Glu Lys Pro Val Lys Pro
 945 950 955 960
 Glu Asn Ser Thr Asp Asn Gly Met Leu Asn Pro Glu Gly Asn Val Gly
 965 970 975

Ser Asp Pro Met Leu Asp Pro Ala Leu Glu Glu Ala Pro Ala Val Asp
 980 985 990
 Pro Val Gln Glu Lys Leu Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly
 995 1000 1005
 Leu Asp Ser Val Ile Phe Asn Met Asp Gly Thr Ile Glu Leu Arg Leu
 1010 1015 1020
 Pro Ser Gly Glu Val Ile Lys Lys Asn Leu Ser Asp Phe Ile Ala
 1025 1030 1035

<210> 3
 <211> 2523
 <212> DNA
 <213> S. pneumoniae

 <220>
 <221> CDS
 <222> (1)...(2520)
 <223> Coding region of BVH-11 gene

<400> 3

atg aaa atc aat aaa aaa tat cta gct ggg tca gta gct aca ctt gtt 48
 Met Lys Ile Asn Lys Lys Tyr Leu Ala Gly Ser Val Ala Thr Leu Val
 1 5 10 15

 tta agt gtc tgt gct tat gaa cta ggt ttg cat caa gct caa act gta 96
 Leu Ser Val Cys Ala Tyr Glu Leu Gly Leu His Gln Ala Gln Thr Val
 20 25 30

 aaa gaa aat aat cgt gtt tcc tat ata gat gga aaa caa gcg acg caa 144
 Lys Glu Asn Asn Arg Val Ser Tyr Ile Asp Gly Lys Gln Ala Thr Gln
 35 40 45

 aaa acg gag aat ttg act cct gat gag gtt agc aag cgt gaa gga atc 192
 Lys Thr Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile
 50 55 60

 aac gcc gaa caa atc gtc atc aag att acg gat caa ggt tat gtg acc 240
 Asn Ala Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr
 65 70 75 80

 tct cat gga gac cat tat cat tac tat aat ggc aag gtc cct tat gat 288
 Ser His Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp
 85 90 95

 gcc atc atc agt gaa gag ctc ctc atg aaa gat ccg aat tat cag ttg 336
 Ala Ile Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu
 100 105 110

 aag gat tca gac att gtc aat gaa atc aag ggt ggt tat gtc att aag 384
 Lys Asp Ser Asp Ile Val Asn Glu Ile Lys Gly Gly Tyr Val Ile Lys
 115 120 125

 gta aac ggt aaa tac tat gtt tac ctt aag gat gca gct cat gcg gat 432
 Val Asn Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp
 130 135 140

aat gtc cgt aca aaa gaa gaa atc aat cgg caa aaa caa gaa cat agt 480
 Asn Val Arg Thr Lys Glu Glu Ile Asn Arg Gln Lys Gln Glu His Ser
 145 150 155 160

cag cat cgt gaa gga ggg act tca gca aac gat ggt gcg gta gcc ttt 528
 Gln His Arg Glu Gly Gly Thr Ser Ala Asn Asp Gly Ala Val Ala Phe
 165 170 175

gca cgt tca cag gga cgc tac acc aca gat gat ggt tat atc ttc aat 576
 Ala Arg Ser Gln Gly Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn
 180 185 190

gca tct gat atc atc gaa gat acg ggc gat gcc tat atc gtt cct cat 624
 Ala Ser Asp Ile Ile Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His
 195 200 205

gga gat cat tac cat tac att cct aag aat gag tta tca gct agc gag 672
 Gly Asp His Tyr His Tyr Ile Pro Lys Asn Glu Leu Ser Ala Ser Glu
 210 215 220

ttg gct gct gca gaa gcc ttc cta tct ggt cgg gaa aat ctg tca aat 720
 Leu Ala Ala Ala Glu Ala Phe Leu Ser Gly Arg Glu Asn Leu Ser Asn
 225 230 235 240

tta aga acc tat cgc cga caa aat agc gat aac act cca aga aca aac 768
 Leu Arg Thr Tyr Arg Arg Gln Asn Ser Asp Asn Thr Pro Arg Thr Asn
 245 250 255

tgg gta cct tct gta agc aat cca gga act aca aat act aac aca agc 816
 Trp Val Pro Ser Val Ser Asn Pro Gly Thr Thr Asn Thr Asn Thr Ser
 260 265 270

aac aac agc aac act aac agt caa gca agt caa agt aat gac att gat 864
 Asn Asn Ser Asn Thr Asn Ser Gln Ala Ser Gln Ser Asn Asp Ile Asp
 275 280 285

agt ctc ttg aaa cag ctc tac aaa ctg cct ttg agt caa cgc cat gta 912
 Ser Leu Leu Lys Gln Leu Tyr Lys Leu Pro Leu Ser Gln Arg His Val
 290 295 300

gaa tct gat ggc ctt att ttc gac cca gcg caa atc aca agt cga acc 960
 Glu Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr
 305 310 315 320

gcc aga ggt gta gct gtc cct cat ggt aac cat tac cac ttt atc cct 1008
 Ala Arg Gly Val Ala Val Pro His Gly Asn His Tyr His Phe Ile Pro
 325 330 335

tat gaa caa atg tct gaa ttg gaa aaa cga att gct cgt att att ccc 1056
 Tyr Glu Gln Met Ser Glu Leu Glu Lys Arg Ile Ala Arg Ile Ile Pro
 340 345 350

ctt cgt tat cgt tca aac cat tgg gta cca gat tca aga cca gaa gaa 1104
 Leu Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Glu
 355 360 365

cca agt cca caa ccg act cca gaa cct agt cca agt ccg caa cct gca 1152
 Pro Ser Pro Gln Pro Thr Pro Glu Pro Ser Pro Ser Pro Gln Pro Ala
 370 375 380

cca aat cct caa cca gct cca agc aat cca att gat gag aaa ttg gtc 1200
 Pro Asn Pro Gln Pro Ala Pro Ser Asn Pro Ile Asp Glu Lys Leu Val
 385 390 395 400

aaa gaa gct gtt cga aaa gta ggc gat ggt tat gtc ttt gag gag aat 1248
 Lys Glu Ala Val Arg Lys Val Gly Asp Gly Tyr Val Phe Glu Glu Asn
 405 410 415

gga gtt tct cgt tat atc cca gcc aag aat ctt tca gca gaa aca gca 1296
 Gly Val Ser Arg Tyr Ile Pro Ala Lys Asn Leu Ser Ala Glu Thr Ala
 420 425 430

gca ggc att gat agc aaa ctg gcc aag cag gaa agt tta tct cat aag 1344
 Ala Gly Ile Asp Ser Lys Leu Ala Lys Gln Glu Ser Leu Ser His Lys
 435 440 445

cta gga gct aag aaa act gac ctc cca tct agt gat cga gaa ttt tac 1392
 Leu Gly Ala Lys Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu Phe Tyr
 450 455 460

aat aag gct tat gac tta cta gca aga att cac caa gat tta ctt gat 1440
 Asn Lys Ala Tyr Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp
 465 470 475 480

aat aaa ggt cga caa gtt gat ttt gag gct ttg gat aac ctg ttg gaa 1488
 Asn Lys Gly Arg Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu
 485 490 495

cga ctc aag gat gtc tca agt gat aaa gtc aag tta gtg gat gat att 1536
 Arg Leu Lys Asp Val Ser Ser Asp Lys Val Lys Leu Val Asp Asp Ile
 500 505 510

ctt gcc ttc tta gct ccg att cgt cat cca gaa cgt tta gga aaa cca 1584
 Leu Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro
 515 520 525

aat gcg caa att acc tac act gat gat gag att caa gta gcc aag ttg 1632
 Asn Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu
 530 535 540

gca ggc aag tac aca aca gaa gac ggt tat atc ttt gat cct cgt gat 1680
 Ala Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp
 545 550 555 560

ata acc agt gat gag ggg gat gcc tat gta act cca cat atg acc cat 1728
 Ile Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His
 565 570 575

agc cac tgg att aaa aaa gat agt ttg tct gaa gct gag aga gcg gca 1776
 Ser His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala
 580 585 590

gcc cag gct tat gct aaa gag aaa ggt ttg acc cct cct tcg aca gac Ala Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp 595 600 605	1824
cat cag gat tca gga aat act gag gca aaa gga gca gaa gct atc tac His Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr 610 615 620	1872
aac cgc gtg aaa gca gct aag aag gtg cca ctt gat cgt atg cct tac Asn Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr 625 630 635 640	1920
aat ctt caa tat act gta gaa gtc aaa aac ggt agt tta atc ata cct Asn Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro 645 650 655	1968
cat tat gac cat tac cat aac atc aaa ttt gag tgg ttt gac gaa ggc His Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly 660 665 670	2016
ctt tat gag gca cct aag ggg tat act ctt gag gat ctt ttg gcg act Leu Tyr Glu Ala Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu Ala Thr 675 680 685	2064
gtc aag tac tat gtc gaa cat cca aac gaa cgt ccg cat tca gat aat Val Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn 690 695 700	2112
ggg ttt ggt aac gct agc gac cat gtt caa aga aac aaa aat ggt caa Gly Phe Gly Asn Ala Ser Asp His Val Gln Arg Asn Lys Asn Gly Gln 705 710 715 720	2160
gct gat acc aat caa acg gaa aaa cca agc gag gag aaa cct cag aca Ala Asp Thr Asn Gln Thr Glu Lys Pro Ser Glu Glu Lys Pro Gln Thr 725 730 735	2208
gaa aaa cct gag gaa gaa acc cct cga gaa gag aaa cca caa agc gag Glu Lys Pro Glu Glu Glu Thr Pro Arg Glu Glu Lys Pro Gln Ser Glu 740 745 750	2256
aaa cca gag tct cca aaa cca aca gag gaa cca gaa gaa gaa tca cca Lys Pro Glu Ser Pro Lys Pro Thr Glu Glu Pro Glu Glu Glu Ser Pro 755 760 765	2304
gag gaa tca gaa gaa cct cag gtc gag act gaa aag gtt gaa gaa aaa Glu Glu Ser Glu Glu Pro Gln Val Glu Thr Glu Lys Val Glu Glu Lys 770 775 780	2352
ctg aga gag gct gaa gat tta ctt gga aaa atc cag gat cca att atc Leu Arg Glu Ala Glu Asp Leu Leu Gly Lys Ile Gln Asp Pro Ile Ile 785 790 795 800	2400
aag tcc aat gcc aaa gag act ctc aca gga tta aaa aat aat tta cta Lys Ser Asn Ala Lys Glu Thr Leu Thr Gly Leu Lys Asn Asn Leu Leu 805 810 815	2448

ttt ggc acc cag gac aac aat act att atg gca gaa gct gaa aaa cta 2496
 Phe Gly Thr Gln Asp Asn Asn Thr Ile Met Ala Glu Ala Glu Lys Leu
 820 825 830

ttg gct tta tta aag gag agt aag taa 2523
 Leu Ala Leu Leu Lys Glu Ser Lys
 835 840

<210> 4
 <211> 840
 <212> PRT
 <213> S. pneumoniae

<400> 4
 Met Lys Ile Asn Lys Lys Tyr Leu Ala Gly Ser Val Ala Thr Leu Val
 1 5 10 15
 Leu Ser Val Cys Ala Tyr Glu Leu Gly Leu His Gln Ala Gln Thr Val
 20 25 30
 Lys Glu Asn Asn Arg Val Ser Tyr Ile Asp Gly Lys Gln Ala Thr Gln
 35 40 45
 Lys Thr Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile
 50 55 60
 Asn Ala Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr
 65 70 75 80
 Ser His Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp
 85 90 95
 Ala Ile Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu
 100 105 110
 Lys Asp Ser Asp Ile Val Asn Glu Ile Lys Gly Gly Tyr Val Ile Lys
 115 120 125
 Val Asn Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp
 130 135 140
 Asn Val Arg Thr Lys Glu Ile Asn Arg Gln Lys Gln Glu His Ser
 145 150 155 160
 Gln His Arg Glu Gly Thr Ser Ala Asn Asp Gly Ala Val Ala Phe
 165 170 175
 Ala Arg Ser Gln Gly Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn
 180 185 190
 Ala Ser Asp Ile Ile Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His
 195 200 205
 Gly Asp His Tyr His Tyr Ile Pro Lys Asn Glu Leu Ser Ala Ser Glu
 210 215 220
 Leu Ala Ala Ala Glu Ala Phe Leu Ser Gly Arg Glu Asn Leu Ser Asn
 225 230 235 240
 Leu Arg Thr Tyr Arg Arg Gln Asn Ser Asp Asn Thr Pro Arg Thr Asn
 245 250 255
 Trp Val Pro Ser Val Ser Asn Pro Gly Thr Thr Asn Thr Asn Thr Ser
 260 265 270
 Asn Asn Ser Asn Thr Asn Ser Gln Ala Ser Gln Ser Asn Asp Ile Asp
 275 280 285
 Ser Leu Leu Lys Gln Leu Tyr Lys Leu Pro Leu Ser Gln Arg His Val
 290 295 300
 Glu Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr
 305 310 315 320
 Ala Arg Gly Val Ala Val Pro His Gly Asn His Tyr His Phe Ile Pro
 325 330 335

Tyr Glu Gln Met Ser Glu Leu Glu Lys Arg Ile Ala Arg Ile Ile Pro
 340 345 350
 Leu Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Glu
 355 360 365
 Pro Ser Pro Gln Pro Thr Pro Glu Pro Ser Pro Ser Pro Gln Pro Ala
 370 375 380
 Pro Asn Pro Gln Pro Ala Pro Ser Asn Pro Ile Asp Glu Lys Leu Val
 385 390 395 400
 Lys Glu Ala Val Arg Lys Val Gly Asp Gly Tyr Val Phe Glu Glu Asn
 405 410 415
 Gly Val Ser Arg Tyr Ile Pro Ala Lys Asn Leu Ser Ala Glu Thr Ala
 420 425 430
 Ala Gly Ile Asp Ser Lys Leu Ala Lys Gln Glu Ser Leu Ser His Lys
 435 440 445
 Leu Gly Ala Lys Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu Phe Tyr
 450 455 460
 Asn Lys Ala Tyr Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp
 465 470 475 480
 Asn Lys Gly Arg Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu
 485 490 495
 Arg Leu Lys Asp Val Ser Ser Asp Lys Val Lys Leu Val Asp Asp Ile
 500 505 510
 Leu Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro
 515 520 525
 Asn Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu
 530 535 540
 Ala Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp
 545 550 555 560
 Ile Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His
 565 570 575
 Ser His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala
 580 585 590
 Ala Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp
 595 600 605
 His Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr
 610 615 620
 Asn Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr
 625 630 635 640
 Asn Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro
 645 650 655
 His Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly
 660 665 670
 Leu Tyr Glu Ala Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu Ala Thr
 675 680 685
 Val Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn
 690 695 700
 Gly Phe Gly Asn Ala Ser Asp His Val Gln Arg Asn Lys Asn Gly Gln
 705 710 715 720
 Ala Asp Thr Asn Gln Thr Glu Lys Pro Ser Glu Glu Lys Pro Gln Thr
 725 730 735
 Glu Lys Pro Glu Glu Glu Thr Pro Arg Glu Glu Lys Pro Gln Ser Glu
 740 745 750
 Lys Pro Glu Ser Pro Lys Pro Thr Glu Glu Pro Glu Glu Ser Pro
 755 760 765
 Glu Glu Ser Glu Glu Pro Gln Val Glu Thr Glu Lys Val Glu Glu Lys
 770 775 780

Leu Arg Glu Ala Glu Asp Leu Leu Gly Lys Ile Gln Asp Pro Ile Ile
 785 790 795 800
 Lys Ser Asn Ala Lys Glu Thr Leu Thr Gly Leu Lys Asn Asn Leu Leu
 805 810 815
 Phe Gly Thr Gln Asp Asn Asn Thr Ile Met Ala Glu Ala Glu Lys Leu
 820 825 830
 Leu Ala Leu Leu Lys Glu Ser Lys
 835 840

<210> 5
 <211> 1581
 <212> DNA
 <213> *S. pneumoniae*

<220>
 <221> CDS
 <222> (1) ... (1578)

<400> 5

atg gag aat ata gac atg ttt aaa tca aat cat gag cga aga atg cgt 48
 Met Glu Asn Ile Asp Met Phe Lys Ser Asn His Glu Arg Arg Met Arg
 1 5 10 15

tat tcc att cgt aaa ttt agt gta gga gta gct agc gta gct gtt gcc 96
 Tyr Ser Ile Arg Lys Phe Ser Val Gly Val Ala Ser Val Ala Val Ala
 20 25 30

agt ctt ttt atg gga agt gtt gta cat gcg aca gag aaa gag gga agt 144
 Ser Leu Phe Met Gly Ser Val Val His Ala Thr Glu Lys Glu Gly Ser
 35 40 45

acc caa gca gcc act tct ttt aat agg gga aat gga agt cag gca gaa 192
 Thr Gln Ala Ala Thr Ser Phe Asn Arg Gly Asn Gly Ser Gln Ala Glu
 50 55 60

caa cgt gga gaa ctc gat tta gaa cga gat aag gca atg aaa gcg gtc 240
 Gln Arg Gly Glu Leu Asp Leu Glu Arg Asp Lys Ala Met Lys Ala Val
 65 70 75 80

agt gaa tat gta gga aaa atg gtg aga gat gcc tat gta aaa tca gat 288
 Ser Glu Tyr Val Gly Lys Met Val Arg Asp Ala Tyr Val Lys Ser Asp
 85 90 95

aga aaa cga cat aaa aat act gta gct cta gtt aac cag ttg gga aac 336
 Arg Lys Arg His Lys Asn Thr Val Ala Leu Val Asn Gln Leu Gly Asn
 100 105 110

att aag aac agg tat ttg aat gaa ata gtt cat tca acc tca aaa agc 384
 Ile Lys Asn Arg Tyr Leu Asn Glu Ile Val His Ser Thr Ser Lys Ser
 115 120 125

caa cta cag gaa ctg atg atg aag agt caa tca gaa gta gat gaa gct 432
 Gln Leu Gln Glu Leu Met Met Lys Ser Gln Ser Glu Val Asp Glu Ala
 130 135 140

gtg tct aaa ttt gaa aag gac tca ttt tct tcg tca agt tca gga tcc 480
Val Ser Lys Phe Glu Lys Asp Ser Phe Ser Ser Ser Ser Gly Ser
145 150 155 160

tcc act aaa cca gaa act ccg cag ccg gaa aat cca gag cat caa aaa 528
Ser Thr Lys Pro Glu Thr Pro Gln Pro Glu Asn Pro Glu His Gln Lys
165 170 175

cca aca act cca tct ccg gat acc aaa cca agc cct caa cca gaa ggc 576
Pro Thr Thr Pro Ser Pro Asp Thr Lys Pro Ser Pro Gln Pro Glu Gly
180 185 190

aag aaa cca agc gta cca gac att aat cag gaa aaa gaa aaa gct aag 624
Lys Lys Pro Ser Val Pro Asp Ile Asn Gln Glu Lys Glu Lys Ala Lys
195 200 205

ctt gct gta gta acc tac atg agc aag att tta gat gat ata caa aaa 672
Leu Ala Val Val Thr Tyr Met Ser Lys Ile Leu Asp Asp Ile Gln Lys
210 215 220

cat cat ctg cag aaa gaa aaa cat cgt cag att gtt gct ctt att aag 720
His His Leu Gln Lys Glu Lys His Arg Gln Ile Val Ala Leu Ile Lys
225 230 235 240

gag ctt gat gag ctt aaa aag caa gct ctt tct gaa att gat aat gta 768
Glu Leu Asp Glu Leu Lys Lys Gln Ala Leu Ser Glu Ile Asp Asn Val
245 250 255

aat acc aaa gta gaa att gaa aat aca gtc cac aag ata ttt gca gac 816
Asn Thr Lys Val Glu Ile Glu Asn Thr Val His Lys Ile Phe Ala Asp
260 265 270

atg gat gca gtt gtg act aaa ttc aaa aaa ggc tta act cag gac aca 864
Met Asp Ala Val Val Thr Lys Phe Lys Lys Gly Leu Thr Gln Asp Thr
275 280 285

cca aaa gaa cca ggt aac aaa aaa cca tct gct cca aaa cca ggt atg 912
Pro Lys Glu Pro Gly Asn Lys Lys Pro Ser Ala Pro Lys Pro Gly Met
290 295 300

caa cca agt cct caa cca gag gtt aaa ccg cag ctg gaa aaa cca aaa 960
Gln Pro Ser Pro Gln Pro Glu Val Lys Pro Gln Leu Glu Lys Pro Lys
305 310 315 320

cca gag gtt aaa ccg caa cca gaa aaa cca aaa cca gag gtt aaa ccg 1008
Pro Glu Val Lys Pro Gln Pro Glu Lys Pro Lys Pro Glu Val Lys Pro
325 330 335

cag ccg gaa aaa cca aaa cca gag gtt aaa ccg cag ccg gaa aaa cca 1056
Gln Pro Glu Lys Pro Lys Pro Glu Val Lys Pro Gln Pro Glu Lys Pro
340 345 350

aaa cca gag gtt aaa ccg cag ccg gaa aaa cca aaa cca gag gtt aaa 1104
Lys Pro Glu Val Lys Pro Gln Pro Glu Lys Pro Lys Pro Glu Val Lys
355 360 365

ccg cag ccg gaa aaa cca aaa cca gag gtt aaa ccg cag ccg gaa aaa 1152
 Pro Gln Pro Glu Lys Pro Lys Pro Glu Val Lys Pro Gln Pro Glu Lys
 370 375 380

cca aaa cca gag gtt aaa ccg cag ccg gaa aaa cca aaa cca gag gtt 1200
 Pro Lys Pro Glu Val Lys Pro Gln Pro Glu Lys Pro Lys Pro Glu Val
 385 390 395 400

aaa ccg cag ccg gaa aaa cca aaa cca gag gtt aaa ccg cag ccg gaa 1248
 Lys Pro Gln Pro Glu Lys Pro Lys Pro Glu Val Lys Pro Gln Pro Glu
 405 410 415

aaa cca aaa cca gag gtt aaa ccg cag ccg gaa aaa cca aaa cca gag 1296
 Lys Pro Lys Pro Glu Val Lys Pro Gln Pro Glu Lys Pro Lys Pro Glu
 420 425 430

gtt aaa ccg caa cca gaa aaa cca aaa cca gag gtt aaa ccg caa cca 1344
 Val Lys Pro Gln Pro Glu Lys Pro Lys Pro Glu Val Lys Pro Gln Pro
 435 440 445

gaa aaa cca aaa cca gat aat agc aag cca caa gca gat gat aag aag 1392
 Glu Lys Pro Lys Pro Asp Asn Ser Lys Pro Gln Ala Asp Asp Lys Lys
 450 455 460

cca tca act aca aat aat tta agc aag gac aag caa cct tct aac caa 1440
 Pro Ser Thr Thr Asn Asn Leu Ser Lys Asp Lys Gln Pro Ser Asn Gln
 465 470 475 480

gct tca aca aac gaa aaa gca aca aat aaa ccg aag aag tca ttg cca 1488
 Ala Ser Thr Asn Glu Lys Ala Thr Asn Lys Pro Lys Lys Ser Leu Pro
 485 490 495

tca act gga tct att tca aat cta gca ctt gaa att gca ggt ctt ctt 1536
 Ser Thr Gly Ser Ile Ser Asn Leu Ala Leu Glu Ile Ala Gly Leu Leu
 500 505 510

acc ttg gcg ggg gca acc att ctt gct aag aaa aga atg aaa 1578
 Thr Leu Ala Gly Ala Thr Ile Leu Ala Lys Lys Arg Met Lys
 515 520 525

tag 1581

<210> 6
 <211> 526
 <212> PRT
 <213> S. pneumoniae

<400> 6
 Met Glu Asn Ile Asp Met Phe Lys Ser Asn His Glu Arg Arg Met Arg
 1 5 10 15
 Tyr Ser Ile Arg Lys Phe Ser Val Gly Val Ala Ser Val Ala Val Ala
 20 25 30
 Ser Leu Phe Met Gly Ser Val Val His Ala Thr Glu Lys Glu Gly Ser
 35 40 45
 Thr Gln Ala Ala Thr Ser Phe Asn Arg Gly Asn Gly Ser Gln Ala Glu
 50 55 60

Gln Arg Gly Glu Leu Asp Leu Glu Arg Asp Lys Ala Met Lys Ala Val
 65 70 75 80
 Ser Glu Tyr Val Gly Lys Met Val Arg Asp Ala Tyr Val Lys Ser Asp
 85 90 95
 Arg Lys Arg His Lys Asn Thr Val Ala Leu Val Asn Gln Leu Gly Asn
 100 105 110
 Ile Lys Asn Arg Tyr Leu Asn Glu Ile Val His Ser Thr Ser Lys Ser
 115 120 125
 Gln Leu Gln Glu Leu Met Met Lys Ser Gln Ser Glu Val Asp Glu Ala
 130 135 140
 Val Ser Lys Phe Glu Lys Asp Ser Phe Ser Ser Ser Ser Ser Gly Ser
 145 150 155 160
 Ser Thr Lys Pro Glu Thr Pro Gln Pro Glu Asn Pro Glu His Gln Lys
 165 170 175
 Pro Thr Thr Pro Ser Pro Asp Thr Lys Pro Ser Pro Gln Pro Glu Gly
 180 185 190
 Lys Lys Pro Ser Val Pro Asp Ile Asn Gln Glu Lys Glu Lys Ala Lys
 195 200 205
 Leu Ala Val Val Thr Tyr Met Ser Lys Ile Leu Asp Asp Ile Gln Lys
 210 215 220
 His His Leu Gln Lys Glu Lys His Arg Gln Ile Val Ala Leu Ile Lys
 225 230 235 240
 Glu Leu Asp Glu Leu Lys Lys Gln Ala Leu Ser Glu Ile Asp Asn Val
 245 250 255
 Asn Thr Lys Val Glu Ile Glu Asn Thr Val His Lys Ile Phe Ala Asp
 260 265 270
 Met Asp Ala Val Val Thr Lys Phe Lys Lys Gly Leu Thr Gln Asp Thr
 275 280 285
 Pro Lys Glu Pro Gly Asn Lys Lys Pro Ser Ala Pro Lys Pro Gly Met
 290 295 300
 Gln Pro Ser Pro Gln Pro Glu Val Lys Pro Gln Leu Glu Lys Pro Lys
 305 310 315 320
 Pro Glu Val Lys Pro Gln Pro Glu Lys Pro Lys Pro Glu Val Lys Pro
 325 330 335
 Gln Pro Glu Lys Pro Lys Pro Glu Val Lys Pro Gln Pro Glu Lys Pro
 340 345 350
 Lys Pro Glu Val Lys Pro Gln Pro Glu Lys Pro Lys Pro Glu Val Lys
 355 360 365
 Pro Gln Pro Glu Lys Pro Lys Pro Glu Val Lys Pro Gln Pro Glu Lys
 370 375 380
 Pro Lys Pro Glu Val Lys Pro Gln Pro Glu Lys Pro Lys Pro Glu Val
 385 390 395 400
 Lys Pro Gln Pro Glu Lys Pro Lys Pro Glu Val Lys Pro Gln Pro Glu
 405 410 415
 Lys Pro Lys Pro Glu Val Lys Pro Gln Pro Glu Lys Pro Lys Pro Glu
 420 425 430
 Val Lys Pro Gln Pro Glu Lys Pro Lys Pro Glu Val Lys Pro Gln Pro
 435 440 445
 Glu Lys Pro Lys Pro Asp Asn Ser Lys Pro Gln Ala Asp Asp Lys Lys
 450 455 460
 Pro Ser Thr Thr Asn Asn Leu Ser Lys Asp Lys Gln Pro Ser Asn Gln
 465 470 475 480
 Ala Ser Thr Asn Glu Lys Ala Thr Asn Lys Pro Lys Lys Ser Leu Pro
 485 490 495
 Ser Thr Gly Ser Ile Ser Asn Leu Ala Leu Glu Ile Ala Gly Leu Leu
 500 505 510

Thr Leu Ala Gly Ala Thr Ile Leu Ala Lys Lys Arg Met Lys
 515 520 525

<210> 7
 <211> 1455
 <212> DNA
 <213> S. pneumoniae

<220>
 <221> CDS
 <222> (1)...(1452)

<400> 7

atg aaa ttt agt aaa aaa tat ata gca gct gga tca gct gtt atc gta 48
 Met Lys Phe Ser Lys Lys Tyr Ile Ala Ala Gly Ser Ala Val Ile Val
 1 5 10 15

tcc ttg agt cta tgt gcc tat gca cta aac cag cat cgt tcg cag gaa 96
 Ser Leu Ser Leu Cys Ala Tyr Ala Leu Asn Gln His Arg Ser Gln Glu
 20 25 30

aat aag gac aat aat cgt gtc tct tat gtg gat ggc agc cag tca agt 144
 Asn Lys Asp Asn Asn Arg Val Ser Tyr Val Asp Gly Ser Gln Ser Ser
 35 40 45

cag aaa agt gaa aac ttg aca cca gac cag gtt agc cag aaa gaa gga 192
 Gln Lys Ser Glu Asn Leu Thr Pro Asp Gln Val Ser Gln Lys Glu Gly
 50 55 60

att cag gct gag caa att gta atc aaa att aca gat cag ggc tat gta 240
 Ile Gln Ala Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val
 65 70 75 80

acg tca cac ggt gac cac tat cat tac tat aat ggg aaa gtt cct tat 288
 Thr Ser His Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr
 85 90 95

gat gcc ctc ttt agt gaa gaa ctc ttg atg aag gat cca aac tat caa 336
 Asp Ala Leu Phe Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln
 100 105 110

ctt aaa gac gct gat att gtc aat gaa gtc aag ggt ggt tat atc atc 384
 Leu Lys Asp Ala Asp Ile Val Asn Glu Val Lys Gly Gly Tyr Ile Ile
 115 120 125

aag gtc gat gga aaa tat tat gtc tac ctg aaa gat gca gct cat gct 432
 Lys Val Asp Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala
 130 135 140

gat aat gtt cga act aaa gat gaa atc aat cgt caa aaa caa gaa cat 480
 Asp Asn Val Arg Thr Lys Asp Glu Ile Asn Arg Gln Lys Gln Glu His
 145 150 155 160

gtc aaa gat aat gag aag gtt aac tct aat gtt gct gta gca agg tct 528
 Val Lys Asp Asn Glu Lys Val Asn Ser Asn Val Ala Val Ala Arg Ser
 165 170 175

cag gga cga tat acg aca aat gat ggt tat gtc ttt aat cca gct gat	576
Gln Gly Arg Tyr Thr Thr Asn Asp Gly Tyr Val Phe Asn Pro Ala Asp	
180 185 190	
att atc gaa gat acg ggt aat gct tat atc gtt cct cat gga ggt cac	624
Ile Ile Glu Asp Thr Gly Asn Ala Tyr Ile Val Pro His Gly Gly His	
195 200 205	
tat cac tac att ccc aaa agc gat tta tct gct agt gaa tta gca gca	672
Tyr His Tyr Ile Pro Lys Ser Asp Leu Ser Ala Ser Glu Leu Ala Ala	
210 215 220	
gct aaa gca cat ctg gct gga aaa aat atg caa ccg agt cag tta agc	720
Ala Lys Ala His Leu Ala Gly Lys Asn Met Gln Pro Ser Gln Leu Ser	
225 230 235 240	
tat tct tca aca gct agt gac aat aac acg caa tct gta gca aaa gga	768
Tyr Ser Ser Thr Ala Ser Asp Asn Asn Thr Gln Ser Val Ala Lys Gly	
245 250 255	
tca act agc aag cca gca aat aaa tct gaa aat ctc cag agt ctt ttg	816
Ser Thr Ser Lys Pro Ala Asn Lys Ser Glu Asn Leu Gln Ser Leu Leu	
260 265 270	
aag gaa ctc tat gat tca cct agc gcc caa cgt tac agt gaa tca gat	864
Lys Glu Leu Tyr Asp Ser Pro Ser Ala Gln Arg Tyr Ser Glu Ser Asp	
275 280 285	
ggc ctg gtc ttt gac cct gct aag att atc agt cgt aca cca aat gga	912
Gly Leu Val Phe Asp Pro Ala Lys Ile Ile Ser Arg Thr Pro Asn Gly	
290 295 300	
gtt gcg att ccg cat ggc gac cat tac cac ttt att cct tac agc aag	960
Val Ala Ile Pro His Gly Asp His Tyr His Phe Ile Pro Tyr Ser Lys	
305 310 315 320	
ctt tct gct tta gaa gaa aag att gcc aga atg gtg cct atc agt gga	1008
Leu Ser Ala Leu Glu Glu Lys Ile Ala Arg Met Val Pro Ile Ser Gly	
325 330 335	
act ggt tct aca gtt tct aca aat gca aaa cct aat gaa gta gtg tct	1056
Thr Gly Ser Thr Val Ser Thr Asn Ala Lys Pro Asn Glu Val Val Ser	
340 345 350	
agt cta ggc agt ctt tca agc aat cct tct tct tta acg aca agt aag	1104
Ser Leu Gly Ser Leu Ser Ser Asn Pro Ser Ser Leu Thr Thr Ser Lys	
355 360 365	
gag ctc tct tca gca tct gat ggt tat att ttt aat cca aaa gat atc	1152
Glu Leu Ser Ser Ala Ser Asp Gly Tyr Ile Phe Asn Pro Lys Asp Ile	
370 375 380	
gtt gaa gaa acg gct aca gct tat att gta aga cat ggt gat cat ttc	1200
Val Glu Glu Thr Ala Thr Ala Tyr Ile Val Arg His Gly Asp His Phe	
385 390 395 400	

cat tac att cca aaa tca aat caa att ggg caa ccg act ctt cca aac	1248
His Tyr Ile Pro Lys Ser Asn Gln Ile Gly Gln Pro Thr Leu Pro Asn	
405 410 415	
aat agt cta gca aca cct tct cca tct ctt cca atc aat cca gga act	1296
Asn Ser Leu Ala Thr Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr	
420 425 430	
tca cat gag aaa cat gaa gaa gat gga tac gga ttt gat gct aat cgt	1344
Ser His Glu Lys His Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg	
435 440 445	
att atc gct gaa gat gaa tca ggt ttt gtc atg agt cac gga gac cac	1392
Ile Ile Ala Glu Asp Glu Ser Gly Phe Val Met Ser His Gly Asp His	
450 455 460	
aat cat tat ttc ttc aag aag gac ttg aca gaa gag caa att aag gtg	1440
Asn His Tyr Phe Phe Lys Lys Asp Leu Thr Glu Glu Gln Ile Lys Val	
465 470 475 480	
cgc aaa aac att tag	1455
Arg Lys Asn Ile	

<210> 8
 <211> 484
 <212> PRT
 <213> S. pneumoniae

<400> 8

Met Lys Phe Ser Lys Lys Tyr Ile Ala Ala Gly Ser Ala Val Ile Val	
1 5 10 15	
Ser Leu Ser Leu Cys Ala Tyr Ala Leu Asn Gln His Arg Ser Gln Glu	
20 25 30	
Asn Lys Asp Asn Asn Arg Val Ser Tyr Val Asp Gly Ser Gln Ser Ser	
35 40 45	
Gln Lys Ser Glu Asn Leu Thr Pro Asp Gln Val Ser Gln Lys Glu Gly	
50 55 60	
Ile Gln Ala Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val	
65 70 75 80	
Thr Ser His Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr	
85 90 95	
Asp Ala Leu Phe Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln	
100 105 110	
Leu Lys Asp Ala Asp Ile Val Asn Glu Val Lys Gly Gly Tyr Ile Ile	
115 120 125	
Lys Val Asp Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala	
130 135 140	
Asp Asn Val Arg Thr Lys Asp Glu Ile Asn Arg Gln Lys Gln Glu His	
145 150 155 160	
Val Lys Asp Asn Glu Lys Val Asn Ser Asn Val Ala Val Ala Arg Ser	
165 170 175	
Gln Gly Arg Tyr Thr Thr Asn Asp Gly Tyr Val Phe Asn Pro Ala Asp	
180 185 190	
Ile Ile Glu Asp Thr Gly Asn Ala Tyr Ile Val Pro His Gly Gly His	
195 200 205	

Tyr His Tyr Ile Pro Lys Ser Asp Leu Ser Ala Ser Glu Leu Ala Ala
 210 215 220
 Ala Lys Ala His Leu Ala Gly Lys Asn Met Gln Pro Ser Gln Leu Ser
 225 230 235 240
 Tyr Ser Ser Thr Ala Ser Asp Asn Asn Thr Gln Ser Val Ala Lys Gly
 245 250 255
 Ser Thr Ser Lys Pro Ala Asn Lys Ser Glu Asn Leu Gln Ser Leu Leu
 260 265 270
 Lys Glu Leu Tyr Asp Ser Pro Ser Ala Gln Arg Tyr Ser Glu Ser Asp
 275 280 285
 Gly Leu Val Phe Asp Pro Ala Lys Ile Ile Ser Arg Thr Pro Asn Gly
 290 295 300
 Val Ala Ile Pro His Gly Asp His Tyr His Phe Ile Pro Tyr Ser Lys
 305 310 315 320
 Leu Ser Ala Leu Glu Glu Lys Ile Ala Arg Met Val Pro Ile Ser Gly
 325 330 335
 Thr Gly Ser Thr Val Ser Thr Asn Ala Lys Pro Asn Glu Val Val Ser
 340 345 350
 Ser Leu Gly Ser Leu Ser Ser Asn Pro Ser Ser Leu Thr Thr Ser Lys
 355 360 365
 Glu Leu Ser Ser Ala Ser Asp Gly Tyr Ile Phe Asn Pro Lys Asp Ile
 370 375 380
 Val Glu Glu Thr Ala Thr Ala Tyr Ile Val Arg His Gly Asp His Phe
 385 390 395 400
 His Tyr Ile Pro Lys Ser Asn Gln Ile Gly Gln Pro Thr Leu Pro Asn
 405 410 415
 Asn Ser Leu Ala Thr Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr
 420 425 430
 Ser His Glu Lys His Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg
 435 440 445
 Ile Ile Ala Glu Asp Glu Ser Gly Phe Val Met Ser His Gly Asp His
 450 455 460
 Asn His Tyr Phe Phe Lys Lys Asp Leu Thr Glu Glu Gln Ile Lys Val
 465 470 475 480
 Arg Lys Asn Ile

<210> 9
 <211> 1587
 <212> DNA
 <213> S pneumoniae

<220>
 <221> CDS
 <222> (1) ... (1584)

<400> 9

atg aaa gat tta gat aaa aaa atc gaa gaa aaa att gct ggc att atg
 Met Lys Asp Leu Asp Lys Lys Ile Glu Glu Lys Ile Ala Gly Ile Met
 1 5 10 15

48

aaa caa tat ggt gtc aaa cgt gaa agt att gtc gtg aat aaa gaa aaa
 Lys Gln Tyr Gly Val Lys Arg Glu Ser Ile Val Val Asn Lys Glu Lys
 20 25 30

96

aat gcg att att tat ccg cat gga gat cac cat cat gca gat ccg att 144
 Asn Ala Ile Ile Tyr Pro His Gly Asp His His His Ala Asp Pro Ile
 35 40 45

gat gaa cat aaa ccg gtt gga att ggt cat tct cac agt aac tat gaa 192
 Asp Glu His Lys Pro Val Gly Ile Gly His Ser His Ser Asn Tyr Glu
 50 55 60

ctg ttt aaa ccc gaa gaa gga gtt gct aaa aaa gaa ggg aat aaa gtt 240
 Leu Phe Lys Pro Glu Glu Gly Val Ala Lys Lys Glu Gly Asn Lys Val
 65 70 75 80

tat act gga gaa gaa tta acg aat gtt gtt aat ttg tta aaa aat agt 288
 Tyr Thr Gly Glu Glu Leu Thr Asn Val Val Asn Leu Leu Lys Asn Ser
 85 90 95

acg ttt aat aat caa aac ttt act cta gcc aat ggt caa aaa cgc gtt 336
 Thr Phe Asn Asn Gln Asn Phe Thr Leu Ala Asn Gly Gln Lys Arg Val
 100 105 110

tct ttt agt ttt ccg cct gaa ttg gag aaa aaa tta ggt atc aat atg 384
 Ser Phe Ser Phe Pro Pro Glu Leu Glu Lys Lys Leu Gly Ile Asn Met
 115 120 125

cta gta aaa tta ata aca cca gat gga aaa gta ttg gag aaa gta tct 432
 Leu Val Lys Leu Ile Thr Pro Asp Gly Lys Val Leu Glu Lys Val Ser
 130 135 140

ggt aaa gta ttt gga gaa gga gta ggg aat att gca aac ttt gaa tta 480
 Gly Lys Val Phe Gly Glu Gly Val Gly Asn Ile Ala Asn Phe Glu Leu
 145 150 155 160

gat caa cct tat tta cca gga caa aca ttt aag tat act atc gct tca 528
 Asp Gln Pro Tyr Leu Pro Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser
 165 170 175

aaa gat tat cca gaa gta agt tat gat ggt aca ttt aca gtt cca acc 576
 Lys Asp Tyr Pro Glu Val Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr
 180 185 190

tct tta gct tac aaa atg gcc agt caa acg att ttc tat cct ttc cat 624
 Ser Leu Ala Tyr Lys Met Ala Ser Gln Thr Ile Phe Tyr Pro Phe His
 195 200 205

gca ggg gat act tat tta aga gtg aac cct caa ttt gca gtg cct aaa 672
 Ala Gly Asp Thr Tyr Leu Arg Val Asn Pro Gln Phe Ala Val Pro Lys
 210 215 220

gga act gat gct tta gtc aga gtg ttt gat gaa ttt cat gga aat gct 720
 Gly Thr Asp Ala Leu Val Arg Val Phe Asp Glu Phe His Gly Asn Ala
 225 230 235 240

tat tta gaa aat aac tat aaa gtt ggt gaa atc aaa tta ccg att ccg 768
 Tyr Leu Glu Asn Asn Tyr Lys Val Gly Glu Ile Lys Leu Pro Ile Pro
 245 250 255

aaa tta aac caa gga aca acc aga acg gcc gga aat aaa att cct gta 816
 Lys Leu Asn Gln Gly Thr Thr Arg Thr Ala Gly Asn Lys Ile Pro Val
 260 265 270

acc ttc atg gca aat gct tat ttg gac aat caa tcg act tat att gtg 864
 Thr Phe Met Ala Asn Ala Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val
 275 280 285

gaa gta cct atc ttg gaa aaa gaa aat caa act gat aaa cca agt att 912
 Glu Val Pro Ile Leu Glu Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile
 290 295 300

cta cca caa ttt aaa agg aat aaa gca caa gaa aac tca aaa ctt gat 960
 Leu Pro Gln Phe Lys Arg Asn Lys Ala Gln Glu Asn Ser Lys Leu Asp
 305 310 315 320

gaa aag gta gaa gaa cca aag act agt gag aag gta gaa aaa gaa aaa 1008
 Glu Lys Val Glu Glu Pro Lys Thr Ser Glu Lys Val Glu Lys Glu Lys
 325 330 335

ctt tct gaa act ggg aat agt act agt aat tca acg tta gaa gaa gtt 1056
 Leu Ser Glu Thr Gly Asn Ser Thr Ser Asn Ser Thr Leu Glu Glu Val
 340 345 350

cct aca gtg gat cct gta caa gaa aaa gta gca aaa ttt gct gaa agt 1104
 Pro Thr Val Asp Pro Val Gln Glu Lys Val Ala Lys Phe Ala Glu Ser
 355 360 365

tat ggg atg aag cta gaa aat gtc ttg ttt aat atg gac gga aca att 1152
 Tyr Gly Met Lys Leu Glu Asn Val Leu Phe Asn Met Asp Gly Thr Ile
 370 375 380

gaa tta tat tta cca tca gga gaa gtc att aaa aag aat atg gca gat 1200
 Glu Leu Tyr Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Met Ala Asp
 385 390 395 400

ttt aca gga gaa gca cct caa gga aat ggt gaa aat aaa cca tct gaa 1248
 Phe Thr Gly Glu Ala Pro Gln Gly Asn Gly Glu Asn Lys Pro Ser Glu
 405 410 415

aat gga aaa gta tct act gga aca gtt gag aac caa cca aca gaa aat 1296
 Asn Gly Lys Val Ser Thr Gly Thr Val Glu Asn Gln Pro Thr Glu Asn
 420 425 430

aaa cca gca gat tct tta cca gag gca cca aac gaa aaa cct gta aaa 1344
 Lys Pro Ala Asp Ser Leu Pro Glu Ala Pro Asn Glu Lys Pro Val Lys
 435 440 445

cca gaa aac tca acg gat aat gga atg ttg aat cca gaa ggg aat gtg 1392
 Pro Glu Asn Ser Thr Asp Asn Gly Met Leu Asn Pro Glu Gly Asn Val
 450 455 460

ggg agt gac cct atg tta gat cca gca tta gag gaa gct cca gca gta 1440
 Glu Ser Asp Pro Met Leu Asp Pro Ala Leu Glu Glu Ala Pro Ala Val
 465 470 475 480

gat cct gta caa gaa aaa tta gaa aaa ttt aca gct agt tac gga tta 1488
 Asp Pro Val Gln Glu Lys Leu Glu Lys Phe Thr Ala Ser Tyr Gly Leu
 485 490 495

ggc tta gat agt gtt ata ttc aat atg gat gga acg att gaa tta aga 1536
 Gly Leu Asp Ser Val Ile Phe Asn Met Asp Gly Thr Ile Glu Leu Arg
 500 505 510

ttg cca agt gga gaa gtg ata aaa aag aat tta tct gat ttc ata gcg 1584
 Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Leu Ser Asp Phe Ile Ala
 515 520 525

taa 1587

<210> 10

<211> 528

<212> PRT

<213> S pneumoniae

<400> 10

Met Lys Asp Leu Asp Lys Lys Ile Glu Glu Lys Ile Ala Gly Ile Met
 1 5 10 15
 Lys Gln Tyr Gly Val Lys Arg Glu Ser Ile Val Val Asn Lys Glu Lys
 20 25 30
 Asn Ala Ile Ile Tyr Pro His Gly Asp His His His Ala Asp Pro Ile
 35 40 45
 Asp Glu His Lys Pro Val Gly Ile Gly His Ser His Ser Asn Tyr Glu
 50 55 60
 Leu Phe Lys Pro Glu Glu Gly Val Ala Lys Lys Glu Gly Asn Lys Val
 65 70 75 80
 Tyr Thr Gly Glu Glu Leu Thr Asn Val Val Asn Leu Leu Lys Asn Ser
 85 90 95
 Thr Phe Asn Asn Gln Asn Phe Thr Leu Ala Asn Gly Gln Lys Arg Val
 100 105 110
 Ser Phe Ser Phe Pro Pro Glu Leu Glu Lys Lys Leu Gly Ile Asn Met
 115 120 125
 Leu Val Lys Leu Ile Thr Pro Asp Gly Lys Val Leu Glu Lys Val Ser
 130 135 140
 Gly Lys Val Phe Gly Glu Gly Val Gly Asn Ile Ala Asn Phe Glu Leu
 145 150 155 160
 Asp Gln Pro Tyr Leu Pro Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser
 165 170 175
 Lys Asp Tyr Pro Glu Val Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr
 180 185 190
 Ser Leu Ala Tyr Lys Met Ala Ser Gln Thr Ile Phe Tyr Pro Phe His
 195 200 205
 Ala Gly Asp Thr Tyr Leu Arg Val Asn Pro Gln Phe Ala Val Pro Lys
 210 215 220
 Gly Thr Asp Ala Leu Val Arg Val Phe Asp Glu Phe His Gly Asn Ala
 225 230 235 240
 Tyr Leu Glu Asn Asn Tyr Lys Val Gly Glu Ile Lys Leu Pro Ile Pro
 245 250 255
 Lys Leu Asn Gln Gly Thr Thr Arg Thr Ala Gly Asn Lys Ile Pro Val
 260 265 270
 Thr Phe Met Ala Asn Ala Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val
 275 280 285

Glu Val Pro Ile Leu Glu Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile
 290 295 300
 Leu Pro Gln Phe Lys Arg Asn Lys Ala Gln Glu Asn Ser Lys Leu Asp
 305 310 315 320
 Glu Lys Val Glu Glu Pro Lys Thr Ser Glu Lys Val Glu Lys Glu Lys
 325 330 335
 Leu Ser Glu Thr Gly Asn Ser Thr Ser Asn Ser Thr Leu Glu Glu Val
 340 345 350
 Pro Thr Val Asp Pro Val Gln Glu Lys Val Ala Lys Phe Ala Glu Ser
 355 360 365
 Tyr Gly Met Lys Leu Glu Asn Val Leu Phe Asn Met Asp Gly Thr Ile
 370 375 380
 Glu Leu Tyr Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Met Ala Asp
 385 390 395 400
 Phe Thr Gly Glu Ala Pro Gln Gly Asn Gly Glu Asn Lys Pro Ser Glu
 405 410 415
 Asn Gly Lys Val Ser Thr Gly Thr Val Glu Asn Gln Pro Thr Glu Asn
 420 425 430
 Lys Pro Ala Asp Ser Leu Pro Glu Ala Pro Asn Glu Lys Pro Val Lys
 435 440 445
 Pro Glu Asn Ser Thr Asp Asn Gly Met Leu Asn Pro Glu Gly Asn Val
 450 455 460
 Gly Ser Asp Pro Met Leu Asp Pro Ala Leu Glu Glu Ala Pro Ala Val
 465 470 475 480
 Asp Pro Val Gln Glu Lys Leu Glu Lys Phe Thr Ala Ser Tyr Gly Leu
 485 490 495
 Gly Leu Asp Ser Val Ile Phe Asn Met Asp Gly Thr Ile Glu Leu Arg
 500 505 510
 Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Leu Ser Asp Phe Ile Ala
 515 520 525

<210> 11


<211> 5048

<212> DNA

<213> *S. pneumoniae*

<400> 11

aattccttgt	cgggtaagtt	ccgacccgca	cgaaaggcgt	aatgatttgg	gcactgtctc	60
aacgagagac	tcggtgaaat	tttagtacct	gtgaagatgc	aggttaccgc	cgacaggacg	120
gaaagacccc	atggagcttt	actgcagttt	gatattgagt	gtctgtacca	catgtacagg	180
ataggtagga	gtctaagaga	tcgggacgcc	agtttcgaag	gagacgctgt	tgggatacta	240
cccttgtgtt	atggccactc	taaccagat	aggatgaccc	tatcggagac	agtgtctgac	300
gggcagtttg	actggggcgg	tcgcctccta	aaaggtaacg	gaggcgccca	aaggttccct	360
cagaatgggt	ggaaatcatt	cgcagagtgt	aaaggataaa	gggagcttga	ctgcgagagc	420
tacaactcga	gcagggacga	aagtcgggct	tagtgatccg	gtggttccgt	atggaagggc	480
catcgctcaa	cggataaaaag	ctaccctggg	gataacaggc	ttatctcccc	caagagttca	540
catcgacggg	gaggtttggc	acctcgatgt	cggctcgtcg	catcctgggg	ctgtagtcgg	600
tcccaagggg	tgggctgttc	gcccattaaa	gcggcacgcg	agctgggttc	agaacgtcgt	660
gagacagttc	ggtccttatc	cgtcgcgggc	gtaggaaatt	tgagaggatc	tgctcctagt	720
acgagaggac	cagagtggac	ttaccgctgg	tgtaccagtt	gtcttgccaa	aggcatcgct	780
gggtagctat	gtaggaaggg	gataaacgct	gaaagcatct	aagtgtgaaa	cccacctcaa	840
gatgagattt	cccatgatta	tatatcagta	agagccctga	gagatgatca	ggtagatagg	900
ttagaagtgg	aagtgtggcg	acacatgtag	cggactaata	ctaatagctc	gaggacttat	960
ccaaagtaac	tgagaatatg	aaagcgaacg	gttttcttaa	attgaataga	tattcaattt	1020
tgagttaggta	ttactcagag	ttaagtgcag	atagcctagg	agatacacct	gtacccatgc	1080
cgaacacaga	agttaagccc	tagaacgccg	gaagtagttg	ggggttgccc	cctgtgagat	1140
agggaagtgc	cttagctcta	gggagtttag	ctcagctggg	agagcatctg	ccttacaagc	1200




agaggggtcag	cggttcgac	ccgttaactc	ccaaaggtcc	cgtagtgtag	cggttatcac	1260
gtcgccctgt	cacggcgaag	atcgcggtt	cgattcccgt	cgggaccgtt	taaggtaacg	1320
caagttat	tagactcgtt	agctcagttg	gtagagcaat	tgacttttaa	tcaatgggtc	1380
actggttcga	gcccagtacg	ggtcataat	gcgggttttg	cggaattcta	atctctttga	1440
aatcatcttc	tctcactttc	caaaactcta	ttacctctta	ttataccaca	tttcaatctt	1500
caacttccca	gtaataataa	cacctctggc	gaaagaagtt	tcaatgtcct	aaagtaataa	1560
gtgaatccaa	ttcaggaact	ccaagaacaa	aagaaacatc	tggtgtcaca	agtattggat	1620
ggcacagagt	cacgtggtag	tctgacccta	gcagaaat	taaatagtaa	actatttact	1680
ggtaatttaa	atggttaaat	aaccggttta	gaaaactatt	taataaagta	aaagaagttg	1740
agaaaaaact	tcatcattta	ttgaaatgag	ggatttatga	aatttagtaa	aaaatatata	1800
gcagctggat	cagctgttat	cgtatccttg	agtctatgtg	cctatgcact	aaaccagcat	1860
cgttcgcagg	aaaataagga	caataatcgt	gtctcttatg	tggtatggcag	ccagtcgaagt	1920
cagaaaagt	aaaacttgac	accagaccag	gttagccaga	aagaagggaat	tcaggctgag	1980
caaattgtaa	tcaaaattac	agatcagggc	tatgtaacgt	cacacgggtga	ccactatcat	2040
tactataatg	ggaaagttcc	ttatgatgcc	ctcttttagtg	aagaactctt	gatgaaggat	2100
ccaaactatc	aacttaaaga	cgctgatatt	gtcaatgaag	tcaaggggtg	ttatatcatc	2160
aaggtcgatg	gaaaatatta	tgtctacctg	aaagatgcag	ctcatgctga	taatgttcga	2220
actaaagatg	aaatcaatcg	tcaaaaacaa	gaacatgtca	aagataatga	gaaggttaac	2280
tctaagtgtg	ctgtagcaag	gtctcagggg	cgatatacga	caaatgatgg	ttatgtcttt	2340
aatccagctg	atattatcga	agatacgggt	aatgccttata	tcgttcctca	tggaaggtcac	2400
tatcactaca	ttcccaaaag	cgatttatct	gctagtgaat	tagcagcagc	taaagcacat	2460
ctggctggaa	aaaatatgca	accgagtcag	ttaagctatt	cttcaacagc	tagtgacaat	2520
aacacgcaat	ctgtagcaaa	aggatcaact	agcaagccag	caaataaatc	tgaaaatctc	2580
cagagtcttt	tgaagggaact	ctatgattca	cctagcgccc	aacgttacag	tgaatcagat	2640
ggcctgggtc	ttgaccctgc	taagattatc	agtcgtacac	caaatggagt	tgcgattccg	2700
catggcgacc	attaccactt	tattccttac	agcaagcttt	ctgctttaga	agaaaagatt	2760
gccagaatgg	tgccatcatg	tggaaactgg	tctacagttt	ctacaaatgc	aaaaccta	2820
gaagtagtgt	ctagtctagg	cagtctttca	agcaatcctt	cttctttaac	gacaagtaag	2880
gagctctctt	cagcatctga	tggttatatt	tttaatccaa	aagatatcgt	tgaagaaacg	2940
gctacagctt	atattgtaag	acatgggtgat	catttccatt	acattccaaa	atcaaatcaa	3000
attgggcaac	cgactcttcc	aaacaatagt	ctagcaacac	cttctccatc	tcttccaatc	3060
aatccaggaa	cttcacatga	gaaacatgaa	gaagatggat	acggatttga	tgctaactgt	3120
attatcgctg	aagatgaatc	aggttttgtc	atgagtcacg	gagaccacaa	tcattatttc	3180
ttcaagaagg	acttgacaga	agagcaaatt	aaggctgcgc	aaaaacattt	agaggaagtt	3240
aaaactagtc	ataatggatt	agattctttg	tcatctcatg	aacaggatta	tccaggtaat	3300
gccaagagaa	tgaagatttt	agataaaaaa	atcgaagaaa	aaattgctgg	cattatgaaa	3360
caatatgggtg	tcaaacgtga	aagtattgtc	tgtaataaag	aaaaaaatgc	gattatttat	3420
ccgcatggag	atcaccatca	tgcagatccg	attgatgaac	ataaaaccgt	tgggaattgg	3480
cattctcaca	gtaactatga	actgtttaaa	cccgaagaag	gagttgctaa	aaaagaaggg	3540
aataaagttt	atactggaga	agaattaacg	aatgttggtt	atttgttaaa	aaatagtacg	3600
tttaataatc	aaaactttac	tctagccaat	ggtcaaaaac	gcgtttcttt	tagttttccg	3660
cctgaattgg	agaaaaaatt	aggatcaat	atgctagtaa	aattaataac	accagatgga	3720
aaagtattgg	agaaagtatc	tggtaaagta	tttggaagag	gagtagggaa	tattgcaaac	3780
tttgaattag	atcaacctta	tttaccagga	caaacattta	agtatactat	cgcttcaaaa	3840
gattatccag	aagtaagtta	tgatggtaca	tttacagttc	caacctcttt	agcttacaaa	3900
atggccagtc	aaacgatttt	ctatcctttc	catgcagggg	atacttattt	aagagtgaac	3960
cctcaatttg	cagtgcctaa	aggaactgat	gctttagtca	gagtgtttga	tgaatttcat	4020
ggaaatgctt	atthagaaaa	taactataaa	gttggtgaaa	tcaaattacc	gattccgaaa	4080
ttaaaccaag	gaacaaccag	aacggccgga	aataaaattc	ctgtaacctt	catggcaaat	4140
gcttatttgg	acaatcaatc	gacttatatt	gtggaagtac	ctatcttgga	aaaagaaaat	4200
caaactgata	aaccaagtat	tctaccacaa	tttaaaagga	ataaagcaca	agaaaaactc	4260
aaacttgatg	aaaaggtaga	agaaccaaag	actagtgaga	aggtagaaaa	agaaaaactt	4320
tctgaaactg	ggaatagtac	tagtaattca	acgttagaag	aagttcctac	agtggtacct	4380
gtacaagaaa	aagtagcaaa	atttgctgat	agttatggga	tgaagctaga	aaatgtcttg	4440
tttaatatgg	acggaacaat	tgaattatat	ttaccatcag	gagaagtcac	taaaaagaat	4500
atggcagatt	ttacaggaga	agcacctcaa	ggaaatgggtg	aaaataaacc	atctgaaaat	4560
ggaaaagtat	ctactggaac	agttgagaac	caaccaacag	aaaataaacc	agcagattct	4620

ttaccagagg	caccaaacga	aaaacctgta	aaaccagaaa	actcaacgga	taatggaatg	4680
ttgaatccag	aaggggaatgt	ggggagtgac	cctatgttag	atccagcatt	agaggaagct	4740
ccagcagtag	atcctgtaca	agaaaaatta	gaaaaattta	cagctagtta	cggattaggg	4800
ttagatagtg	ttatattcaa	tatggatgga	acgattgaat	taagattgcc	aagtggagaa	4860
gtgataaaaa	agaattttatc	tgattttcata	gcgtaaggaa	tagcagtaga	aaaagtctga	4920
atcaaaaatg	aagttctctc	aaaagttaga	aataaaaactc	tgactttggg	agaatttcat	4980
tttattatta	atatataaaa	tttcttgaca	tacaacttaa	aaagaggtgg	aatattttact	5040
agttaatt						5048

<210> 12
 <211> 2647
 <212> DNA
 <213> *S. pneumoniae*

<400> 12



cagagatctt	agtgaatcaa	atatacttaa	gaaaagagga	aagaatgaaa	atcaataaaa	60
aatatctagc	tgggtcagta	gctacacttg	ttttaagtgt	ctgtgcttat	gaactaggtt	120
tgcatcaagc	tcaaactgta	aaagaaaata	atcgtgtttc	ctatatagat	ggaaaacaag	180
cgacgcaaaa	aacggagaat	ttgactcctg	atgaggttag	caagcgtgaa	ggaatcaacg	240
ccgaacaaat	cgtcatcaag	attacggatc	aagggttatgt	gacctctcat	ggagaccatt	300
atcattacta	taatggcaag	gtcccttatg	atgccatcat	cagtgaagag	ctcctcatga	360
aagatccgaa	ttatcagttg	aaggattcag	acattgtcaa	tgaaatcaag	ggtggttatg	420
tcattaaggt	aaacggtaaa	tactatgttt	accttaagga	tgacgctcat	gcggataatg	480
tccgtacaaa	agaagaaatc	aatcggcaaa	aacaagaaca	tagtcagcat	cgtgaaggag	540
ggacttcagc	aaacgatggg	gcggtagcct	ttgcacgttc	acagggacgc	tacaccacag	600
atgatgggta	tatcttcaat	gcattctgata	tcacgaaga	tacgggcat	gcctatatcg	660
ttcctcatgg	agatcattac	cattacattc	ctaagaatga	gttatcagct	agcaggttgg	720
ctgctgcaga	agccttccta	tctggtcggg	aaaatctgtc	aaatttaaga	acctatcgcc	780
gacaaaatag	cgataacact	ccaagaacaa	actgggtacc	ttctgtaagc	aatccaggaa	840
ctacaaatac	taacacaagc	aacaacagca	acactaacag	tcaagcaagt	caaagtaatg	900
acattgatag	tctcttgaaa	cagctctaca	aactgccttt	gagtcaacgc	catgtagaat	960
ctgatggcct	tattttcgac	ccagcgcaaa	tcacaagtcg	aaccgccaga	ggtgtagctg	1020
tccctcatgg	taaccattac	cacttttatcc	cttatgaaca	aatgtctgaa	ttggaaaaaac	1080
gaattgctcg	tattattccc	cttcgtttatc	gttcaaacca	ttgggtacca	gattcaagac	1140
cagaagaacc	aagtcacaaa	ccgactccag	aacctagtc	aagtcgcaa	cctgcaccaa	1200
atcctcaacc	agctccaagc	aatccaattg	atgagaatt	ggtcaaagaa	cctggttcgaa	1260
aagtaggcga	tggttatgtc	tttgaggaga	atggagtttc	tcgttatatc	ccagccaaga	1320
atctttcagc	agaaacagca	gcaggcattg	atagcaaact	ggccaagcag	gaaagtttat	1380
ctcataagct	aggagctaag	aaaactgacc	tcccatctag	tgatcgagaa	ttttacaata	1440
aggcttatga	cttactagca	agaattcacc	aagattttact	tgataataaa	ggtcgacaag	1500
ttgattttga	ggctttggat	aacctgttgg	aacgactcaa	ggatgtctca	agtataaaag	1560
tcaagttagt	ggatgatatt	cttgcccttct	tagctccgat	tcgtcatcca	gaacgttttag	1620
gaaaacaaa	tgcgcaaatt	acctacactg	atgatgagat	tcaagtagcc	aagttggcag	1680
gcaagtacac	aacagaagac	ggttatatct	ttgatcctcg	tgatataacc	agtgatgagg	1740
gggatgccta	tgtaactcca	catatgacct	atagccactg	gattaaaaaa	gatagtttgt	1800
ctgaagctga	gagagcggca	gcccaggctt	atgctaaaga	gaaagggttg	acccctcctt	1860
cgacagacca	tcaggattca	ggaaatactg	aggcaaaagg	agcagaagct	atctacaacc	1920
gcgtgaaagc	agctaagaag	gtgccacttg	atcgtatgcc	ttacaatctt	caatatactg	1980
tagaagtcaa	aaacggtagt	ttaatcatac	ctcattatga	ccattaccat	aacatcaaat	2040
ttgagtgggt	tgacgaaggc	ctttatgagg	cacctaaagg	gtatactctt	gaggatcttt	2100
tggcgactgt	caagtactat	gtcgaacatc	caaacgaacg	tccgcattca	gataatgggt	2160
ttggtaacgc	tagcgaccat	gttcaaagaa	acaaaaatgg	tcaagctgat	accaatcaaa	2220
cggaaaaacc	aagcgaggag	aaacctcaga	cagaaaaacc	tgaggaagaa	acccctcgag	2280
aagagaaaacc	acaaagcgag	aaaccagagt	ctccaaaacc	aacagaggaa	ccagaagaag	2340
aatcaccaga	ggaatcagaa	gaacctcagg	tcgagactga	aaaggttgaa	gaaaaactga	2400

gagaggctga agatttactt ggaaaaatcc aggatccaat tatcaagtcc aatgccaaag 2460
 agactctcac aggattaaaa aataatttac tatttggcac ccaggacaac aatactatta 2520
 tggcagaagc tgaaaaacta ttggctttat taaaggagag taagtaaagg tagcagcatt 2580
 ttctaactcc taaaaacagg ataggagaac gggaaaacga aaaatgagag cagaatgtga 2640
 gttctag 2647

<210> 13
 <211> 2639
 <212> DNA
 <213> *S. pneumoniae*

<220>
 <221> CDS
 <222> (114)...(2627)

<400> 13
 gggctcttaaa actctgaatc ctttagaggc agaccacaaa aatgacaaga cctatttaga 60
 aaatctggaa gaaaatatga gtgttctagc agaagaatta aagtgaggaa aga atg 116
 Met
 1

aaa atc aat aaa aaa tat cta gca ggt tca gtg gca gtc ctt gcc cta 164
 Lys Ile Asn Lys Lys Tyr Leu Ala Gly Ser Val Ala Val Leu Ala Leu
 5 10 15

agt gtt tgt tcc tat gaa ctt ggt cgt cac caa gct ggt cag gtt aag 212
 Ser Val Cys Ser Tyr Glu Leu Gly Arg His Gln Ala Gly Gln Val Lys
 20 25 30

aaa gag tct aat cga gtt tct tat ata gat ggt gat cag gct ggt caa 260
 Lys Glu Ser Asn Arg Val Ser Tyr Ile Asp Gly Asp Gln Ala Gly Gln
 35 40 45

aag gca gaa aat ttg aca cca gat gaa gtc agt aag aga gag ggg atc 308
 Lys Ala Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile
 50 55 60 65

aac gcc gaa caa att gtt atc aag att acg gat caa ggt tat gtg acc 356
 Asn Ala Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr
 70 75 80

tct cat gga gac cat tat cat tac tat aat ggc aag gtt cct tat gat 404
 Ser His Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp
 85 90 95

gcc atc atc agt gaa gaa ctt ctc atg aaa gat ccg aat tat cag ttg 452
 Ala Ile Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu
 100 105 110

aag gat tca gac att gtc aat gaa atc aag ggt ggc tat gtg att aag 500
 Lys Asp Ser Asp Ile Val Asn Glu Ile Lys Gly Gly Tyr Val Ile Lys
 115 120 125

gta gac gga aaa tac tat gtt tac ctt aaa gat gcg gcc cat gcg gac 548
 Val Asp Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp
 130 135 140 145

aat att cgg aca aaa gaa gag att aaa cgt cag aag cag gaa cac agt 596
 Asn Ile Arg Thr Lys Glu Glu Ile Lys Arg Gln Lys Gln Glu His Ser
 150 155 160

cat aat cat aac tca aga gca gat aat gct gtt gct gca gcc aga gcc 644
 His Asn His Asn Ser Arg Ala Asp Asn Ala Val Ala Ala Ala Arg Ala
 165 170 175

caa gga cgt tat aca acg gat gat ggg tat atc ttc aat gca tct gat 692
 Gln Gly Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser Asp
 180 185 190

atc att gag gac acg ggt gat gct tat atc gtt cct cac ggc gac cat 740
 Ile Ile Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asp His
 195 200 205

tac cat tac att cct aag aat gag tta tca gct agc gag tta gct gct 788
 Tyr His Tyr Ile Pro Lys Asn Glu Leu Ser Ala Ser Glu Leu Ala Ala
 210 215 220 225

gca gaa gcc tat tgg aat ggg aag cag gga tct cgt cct tct tca agt 836
 Ala Glu Ala Tyr Trp Asn Gly Lys Gln Gly Ser Arg Pro Ser Ser Ser
 230 235 240

tct agt tat aat gca aat cca gtt caa cca aga ttg tca gag aac cac 884
 Ser Ser Tyr Asn Ala Asn Pro Val Gln Pro Arg Leu Ser Glu Asn His
 245 250 255

aat ctg act gtc act cca act tat cat caa aat caa ggg gaa aac att 932
 Asn Leu Thr Val Thr Pro Thr Tyr His Gln Asn Gln Gly Glu Asn Ile
 260 265 270

tca agc ctt tta cgt gaa ttg tat gct aaa ccc tta tca gaa cgc cat 980
 Ser Ser Leu Leu Arg Glu Leu Tyr Ala Lys Pro Leu Ser Glu Arg His
 275 280 285

gta gaa tct gat ggc ctt att ttc gac cca gcg caa atc aca agt cga 1028
 Val Glu Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser Arg
 290 295 300 305

acc gcc aga ggt gta gct gtc cct cat ggt aac cat tac cac ttt atc 1076
 Thr Ala Arg Gly Val Ala Val Pro His Gly Asn His Tyr His Phe Ile
 310 315 320

cct tat gaa caa atg tct gaa ttg gaa aaa cga att gct cgt att att 1124
 Pro Tyr Glu Gln Met Ser Glu Leu Glu Lys Arg Ile Ala Arg Ile Ile
 325 330 335

ccc ctt cgt tat cgt tca aac cat tgg gta cca gat tca aga cca gaa 1172
 Pro Leu Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu
 340 345 350

caa cca agt cca caa tcg act ccg gaa cct agt cca agt ctg caa cct 1220
 Gln Pro Ser Pro Gln Ser Thr Pro Glu Pro Ser Pro Ser Leu Gln Pro
 355 360 365

gca cca aat cct caa cca gct cca agc aat cca att gat gag aaa ttg 1268
 Ala Pro Asn Pro Gln Pro Ala Pro Ser Asn Pro Ile Asp Glu Lys Leu
 370 375 380 385

gtc aaa gaa gct gtt cga aaa gta ggc gat ggt tat gtc ttt gag gag 1316
 Val Lys Glu Ala Val Arg Lys Val Gly Asp Gly Tyr Val Phe Glu Glu
 390 395 400

aat gga gtt tct cgt tat atc cca gcc aag gat ctt tca gca gaa aca 1364
 Asn Gly Val Ser Arg Tyr Ile Pro Ala Lys Asp Leu Ser Ala Glu Thr
 405 410 415

gca gca ggc att gat agc aaa ctg gcc aag cag gaa agt tta tct cat 1412
 Ala Ala Gly Ile Asp Ser Lys Leu Ala Lys Gln Glu Ser Leu Ser His
 420 425 430

aag cta gga gct aag aaa act gac ctc cca tct agt gat cga gaa ttt 1460
 Lys Leu Gly Ala Lys Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu Phe
 435 440 445

tac aat aag gct tat gac tta cta gca aga att cac caa gat tta ctt 1508
 Tyr Asn Lys Ala Tyr Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu
 450 455 460 465

gat aat aaa ggt cga caa gtt gat ttt gag gtt ttg gat aac ctg ttg 1556
 Asp Asn Lys Gly Arg Gln Val Asp Phe Glu Val Leu Asp Asn Leu Leu
 470 475 480

gaa cga ctc aag gat gtc tca agt gat aaa gtc aag tta gtg gat gat 1604
 Glu Arg Leu Lys Asp Val Ser Ser Asp Lys Val Lys Leu Val Asp Asp
 485 490 495

att ctt gcc ttc tta gct ccg att cgt cat cca gaa cgt tta gga aaa 1652
 Ile Leu Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys
 500 505 510

cca aat gcg caa att acc tac act gat gat gag att caa gta gcc aag 1700
 Pro Asn Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys
 515 520 525

ttg gca ggc aag tac aca aca gaa gac ggt tat atc ttt gat cct cgt 1748
 Leu Ala Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg
 530 535 540 545

gat ata acc agt gat gag ggg gat gcc tat gta act cca cat atg acc 1796
 Asp Ile Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr
 550 555 560

cat agc cac tgg att aaa aaa gat agt ttg tct gaa gct gag aga gcg 1844
 His Ser His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala
 565 570 575

gca gcc cag gct tat gct aaa gag aaa ggt ttg acc cct cct tcg aca 1892
 Ala Ala Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr
 580 585 590

gac cac cag gat tca gga aat act gag gca aaa gga gca gaa gct atc Asp His Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile 595 600 605	1940
tac aac cgc gtg aaa gca gct aag aag gtg cca ctt gat cgt atg cct Tyr Asn Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro 610 615 620 625	1988
tac aat ctt caa tat act gta gaa gtc aaa aac ggt agt tta atc ata Tyr Asn Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile 630 635 640	2036
cct cat tat gac cat tac cat aac atc aaa ttt gag tgg ttt gac gaa Pro His Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu 645 650 655	2084
ggc ctt tat gag gca cct aag ggg tat agt ctt gag gat ctt ttg gcg Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala 660 665 670	2132
act gtc aag tac tat gtc gaa cat cca aac gaa cgt ccg cat tca gat Thr Val Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His Ser Asp 675 680 685	2180
aat ggt ttt ggt aac gct agt gac cat gtt cgt aaa aat aag gca gac Asn Gly Phe Gly Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp 690 695 700 705	2228
caa gat agt aaa cct gat gaa gat aag gaa cat gat gaa gta agt gag Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu 710 715 720	2276
cca act cac cct gaa tct gat gaa aaa gag aat cac gct ggt tta aat Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn 725 730 735	2324
cct tca gca gat aat ctt tat aaa cca agc act gat acg gaa gag aca Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr 740 745 750	2372
gag gaa gaa gct gaa gat acc aca gat gag gct gaa att cct caa gta Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gln Val 755 760 765	2420
gag aat tct gtt att aac gct aag ata gca gat gcg gag gcc ttg cta Glu Asn Ser Val Ile Asn Ala Lys Ile Ala Asp Ala Glu Ala Leu Leu 770 775 780 785	2468
gaa aaa gta aca gat cct agt att aga caa aat gct atg gag aca ttg Glu Lys Val Thr Asp Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu 790 795 800	2516
act ggt cta aaa agt agt ctt ctt ctc gga acg aaa gat aat aac act Thr Gly Leu Lys Ser Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr 805 810 815	2564

att tca gca gaa gta gat agt ctc ttg gct ttg tta aaa gaa agt caa 2612
 Ile Ser Ala Glu Val Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln
 820 825 830

ccg gct cct ata cag tagtaaaatg aa 2639
 Pro Ala Pro Ile Gln
 835

<210> 14
 <211> 838
 <212> PRT
 <213> S. pneumoniae

<400> 14
 Met Lys Ile Asn Lys Lys Tyr Leu Ala Gly Ser Val Ala Val Leu Ala
 1 5 10 15
 Leu Ser Val Cys Ser Tyr Glu Leu Gly Arg His Gln Ala Gly Gln Val
 20 25 30
 Lys Lys Glu Ser Asn Arg Val Ser Tyr Ile Asp Gly Asp Gln Ala Gly
 35 40 45
 Gln Lys Ala Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly
 50 55 60
 Ile Asn Ala Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val
 65 70 75 80
 Thr Ser His Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr
 85 90 95
 Asp Ala Ile Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln
 100 105 110
 Leu Lys Asp Ser Asp Ile Val Asn Glu Ile Lys Gly Gly Tyr Val Ile
 115 120 125
 Lys Val Asp Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala
 130 135 140
 Asp Asn Ile Arg Thr Lys Glu Glu Ile Lys Arg Gln Lys Gln Glu His
 145 150 155 160
 Ser His Asn His Asn Ser Arg Ala Asp Asn Ala Val Ala Ala Ala Arg
 165 170 175
 Ala Gln Gly Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser
 180 185 190
 Asp Ile Ile Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asp
 195 200 205
 His Tyr His Tyr Ile Pro Lys Asn Glu Leu Ser Ala Ser Glu Leu Ala
 210 215 220
 Ala Ala Glu Ala Tyr Trp Asn Gly Lys Gln Gly Ser Arg Pro Ser Ser
 225 230 235 240
 Ser Ser Ser Tyr Asn Ala Asn Pro Val Gln Pro Arg Leu Ser Glu Asn
 245 250 255
 His Asn Leu Thr Val Thr Pro Thr Tyr His Gln Asn Gln Gly Glu Asn
 260 265 270
 Ile Ser Ser Leu Leu Arg Glu Leu Tyr Ala Lys Pro Leu Ser Glu Arg
 275 280 285
 His Val Glu Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser
 290 295 300
 Arg Thr Ala Arg Gly Val Ala Val Pro His Gly Asn His Tyr His Phe
 305 310 315 320
 Ile Pro Tyr Glu Gln Met Ser Glu Leu Glu Lys Arg Ile Ala Arg Ile
 325 330 335

Ile Pro Leu Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro
 340 345 350
 Glu Gln Pro Ser Pro Gln Ser Thr Pro Glu Pro Ser Pro Ser Leu Gln
 355 360 365
 Pro Ala Pro Asn Pro Gln Pro Ala Pro Ser Asn Pro Ile Asp Glu Lys
 370 375 380
 Leu Val Lys Glu Ala Val Arg Lys Val Gly Asp Gly Tyr Val Phe Glu
 385 390 395 400
 Glu Asn Gly Val Ser Arg Tyr Ile Pro Ala Lys Asp Leu Ser Ala Glu
 405 410 415
 Thr Ala Ala Gly Ile Asp Ser Lys Leu Ala Lys Gln Glu Ser Leu Ser
 420 425 430
 His Lys Leu Gly Ala Lys Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu
 435 440 445
 Phe Tyr Asn Lys Ala Tyr Asp Leu Leu Ala Arg Ile His Gln Asp Leu
 450 455 460
 Leu Asp Asn Lys Gly Arg Gln Val Asp Phe Glu Val Leu Asp Asn Leu
 465 470 475 480
 Leu Glu Arg Leu Lys Asp Val Ser Ser Asp Lys Val Lys Leu Val Asp
 485 490 495
 Asp Ile Leu Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg Leu Gly
 500 505 510
 Lys Pro Asn Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala
 515 520 525
 Lys Leu Ala Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro
 530 535 540
 Arg Asp Ile Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met
 545 550 555 560
 Thr His Ser His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg
 565 570 575
 Ala Ala Ala Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser
 580 585 590
 Thr Asp His Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala
 595 600 605
 Ile Tyr Asn Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met
 610 615 620
 Pro Tyr Asn Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile
 625 630 635 640
 Ile Pro His Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp
 645 650 655
 Glu Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu
 660 665 670
 Ala Thr Val Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His Ser
 675 680 685
 Asp Asn Gly Phe Gly Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala
 690 695 700
 Asp Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser
 705 710 715 720
 Glu Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu
 725 730 735
 Asn Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu
 740 745 750
 Thr Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gln
 755 760 765
 Val Glu Asn Ser Val Ile Asn Ala Lys Ile Ala Asp Ala Glu Ala Leu
 770 775 780

Leu Glu Lys Val Thr Asp Pro Ser Ile Arg Gln Asn Ala Met Glu Thr
 785 790 795 800
 Leu Thr Gly Leu Lys Ser Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn
 805 810 815
 Thr Ile Ser Ala Glu Val Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser
 820 825 830
 Gln Pro Ala Pro Ile Gln
 835

<210> 15
 <211> 2528
 <212> DNA
 <213> S. pneumoniae

<220>
 <221> CDS
 <222> (1) ... (2520)

<400> 15

tgt gcc tat gca cta aac cag cat cgt tcg cag gaa aat aag gac aat 48
 Cys Ala Tyr Ala Leu Asn Gln His Arg Ser Gln Glu Asn Lys Asp Asn
 1 5 10 15

aat cgt gtc tct tat gtg gat ggc agc cag tca agt cag aaa agt gaa 96
 Asn Arg Val Ser Tyr Val Asp Gly Ser Gln Ser Ser Gln Lys Ser Glu
 20 25 30

aac ttg aca cca gac cag gtt agc cag aaa gaa gga att cag gct gag 144
 Asn Leu Thr Pro Asp Gln Val Ser Gln Lys Glu Gly Ile Gln Ala Glu
 35 40 45

caa att gta atc aaa att aca gat cag ggc tat gta acg tca cac ggt 192
 Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly
 50 55 60

gat cac tat cat tac tat aat ggg aaa gtt cct tat gat gcc ctc ttt 240
 Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Leu Phe
 65 70 75 80

agt gaa gaa ctc ttg atg aag gat cca aac tat caa ctt aaa gac gct 288
 Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp Ala
 85 90 95

gat att gtc aat gaa gtc aag ggt ggt tat atc atc aag gtc gat gga 336
 Asp Ile Val Asn Glu Val Lys Gly Gly Tyr Ile Ile Lys Val Asp Gly
 100 105 110

aaa tat tat gtc tac ctg aaa gat gca gct cat gct gat aat gtt cga 384
 Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg
 115 120 125

act aaa gat gaa atc aat cgt caa aaa caa gaa cat gtc aaa gat aat 432
 Thr Lys Asp Glu Ile Asn Arg Gln Lys Gln Glu His Val Lys Asp Asn
 130 135 140

gag aag gtt aac tct aat gtt gct gta gca agg tct cag gga cga tat 480
 Glu Lys Val Asn Ser Asn Val Ala Val Ala Arg Ser Gln Gly Arg Tyr
 145 150 155 160

acg aca aat gat ggt tat gtc ttt aat cca gct gat att atc gaa gat 528
 Thr Thr Asn Asp Gly Tyr Val Phe Asn Pro Ala Asp Ile Ile Glu Asp
 165 170 175

acg ggt aat gct tat atc gtt cct cat gga ggt cac tat cac tac att 576
 Thr Gly Asn Ala Tyr Ile Val Pro His Gly Gly His Tyr His Tyr Ile
 180 185 190

ccc aaa agc gat tta tct gct agt gaa tta gca gca gct aaa gca cat 624
 Pro Lys Ser Asp Leu Ser Ala Ser Glu Leu Ala Ala Ala Lys Ala His
 195 200 205

ctg gct gga aaa aat atg caa ccg agt cag tta agc tat tct tca aca 672
 Leu Ala Gly Lys Asn Met Gln Pro Ser Gln Leu Ser Tyr Ser Ser Thr
 210 215 220

cct tct cca tct ctt cca atc aat cca gga act tca cat gag aaa cat 720
 Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His
 225 230 235 240

gaa gaa gat gga tac gga ttt gat gct aat cgt att atc gct gaa gat 768
 Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp
 245 250 255

gaa tca ggt ttt gtc atg agt cac gga gac cac aat cat tat ttc ttc 816
 Glu Ser Gly Phe Val Met Ser His Gly Asp His Asn His Tyr Phe Phe
 260 265 270

aag aag gac ttg aca gaa gag caa att aag gct gcg caa aaa cat tta 864
 Lys Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu
 275 280 285

gag gaa gtt aaa act agt cat aat gga tta gat tct ttg tca tct cat 912
 Glu Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His
 290 295 300

gaa cag gat tat cca agt aat gcc aaa gaa atg aaa gat tta gat aaa 960
 Glu Gln Asp Tyr Pro Ser Asn Ala Lys Glu Met Lys Asp Leu Asp Lys
 305 310 315 320

aaa atc gaa gaa aaa att gct ggc att atg aaa caa tat ggt gtc aaa 1008
 Lys Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys
 325 330 335

cgt gaa agt att gtc gtg aat aaa gaa aaa aat gcg att att tat ccg 1056
 Arg Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro
 340 345 350

cat gga gat cac cat cat gca gat ccg att gat gaa cat aaa ccg gtt 1104
 His Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro Val
 355 360 365

gga att ggt cat tct cac agt aac tat gaa ctg ttt aaa ccc gaa gaa 1152
 Gly Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu
 370 375 380

gga gtt gct aaa aaa gaa ggg aat aaa gtt tat act gga gaa gaa tta 1200
 Gly Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu
 385 390 395 400

acg aat gtt gtt aat ttg tta aaa aat agt acg ttt aat aat caa aac 1248
 Thr Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn
 405 410 415

ttt act cta gcc aat ggt caa aaa cgc gtt tct ttt agt ttt ccg cct 1296
 Phe Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro
 420 425 430

gaa ttg gag aaa aaa tta ggt atc aat atg cta gta aaa tta ata aca 1344
 Glu Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr
 435 440 445

cca gat gga aaa gta ttg gag aaa gta tct ggt aaa gta ttt gga gaa 1392
 Pro Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu
 450 455 460

gga gta ggg aat att gca aac ttt gaa tta gat caa cct tat tta cca 1440
 Gly Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro
 465 470 475 480

gga caa aca ttt aag tat act atc gct tca aaa gat tat cca gaa gta 1488
 Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val
 485 490 495

agt tat gat ggt aca ttt aca gtt cca acc tct tta gct tac aaa atg 1536
 Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met
 500 505 510

gcc agt caa acg att ttc tat cct ttc cat gca ggg gat act tat tta 1584
 Ala Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu
 515 520 525

aga gtg aac cct caa ttt gca gtg cct aaa gga act gat gct tta gtc 1632
 Arg Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val
 530 535 540

aga gtg ttt gat gaa ttt cat gga aat gct tat tta gaa aat aac tat 1680
 Arg Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr
 545 550 555 560

aaa gtt ggt gaa atc aaa tta ccg att ccg aaa tta aac caa gga aca 1728
 Lys Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr
 565 570 575

acc aga acg gcc gga aat aaa att cct gta acc ttc atg gca aat gct 1776
 Thr Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala
 580 585 590

tat	ttg	gac	aat	caa	tcg	act	tat	att	gtg	gaa	gta	cct	atc	ttg	gaa	1824
Tyr	Leu	Asp	Asn	Gln	Ser	Thr	Tyr	Ile	Val	Glu	Val	Pro	Ile	Leu	Glu	
		595					600					605				
aaa	gaa	aat	caa	act	gat	aaa	cca	agt	att	cta	cca	caa	ttt	aaa	agg	1872
Lys	Glu	Asn	Gln	Thr	Asp	Lys	Pro	Ser	Ile	Leu	Pro	Gln	Phe	Lys	Arg	
	610					615					620					
aat	aaa	gca	caa	gaa	aac	tca	aaa	ctt	gat	gaa	aag	gta	gaa	gaa	cca	1920
Asn	Lys	Ala	Gln	Glu	Asn	Ser	Lys	Leu	Asp	Glu	Lys	Val	Glu	Glu	Pro	
625					630					635					640	
aag	act	agt	gag	aag	gta	gaa	aaa	gaa	aaa	ctt	tct	gaa	act	ggg	aat	1968
Lys	Thr	Ser	Glu	Lys	Val	Glu	Lys	Glu	Lys	Leu	Ser	Glu	Thr	Gly	Asn	
			645					650						655		
agt	act	agt	aat	tca	acg	tta	gaa	gaa	gtt	cct	aca	gtg	gat	cct	gta	2016
Ser	Thr	Ser	Asn	Ser	Thr	Leu	Glu	Glu	Val	Pro	Thr	Val	Asp	Pro	Val	
			660					665						670		
caa	gaa	aaa	gta	gca	aaa	ttt	gct	gaa	agt	tat	ggg	atg	aag	cta	gaa	2064
Gln	Glu	Lys	Val	Ala	Lys	Phe	Ala	Glu	Ser	Tyr	Gly	Met	Lys	Leu	Glu	
		675					680					685				
aat	gtc	ttg	ttt	aat	atg	gac	gga	aca	att	gaa	tta	tat	tta	cca	tcg	2112
Asn	Val	Leu	Phe	Asn	Met	Asp	Gly	Thr	Ile	Glu	Leu	Tyr	Leu	Pro	Ser	
		690				695						700				
gga	gaa	gtc	att	aaa	aag	aat	atg	gca	gat	ttt	aca	gga	gaa	gca	cct	2160
Gly	Glu	Val	Ile	Lys	Lys	Asn	Met	Ala	Asp	Phe	Thr	Gly	Glu	Ala	Pro	
705					710					715					720	
caa	gga	aat	ggt	gaa	aat	aaa	cca	tct	gaa	aat	gga	aaa	gta	tct	act	2208
Gln	Gly	Asn	Gly	Glu	Asn	Lys	Pro	Ser	Glu	Asn	Gly	Lys	Val	Ser	Thr	
			725						730					735		
gga	aca	gtt	gag	aac	caa	cca	aca	gaa	aat	aaa	cca	gca	gat	tct	tta	2256
Gly	Thr	Val	Glu	Asn	Gln	Pro	Thr	Glu	Asn	Lys	Pro	Ala	Asp	Ser	Leu	
			740					745					750			
cca	gag	gca	cca	aac	gaa	aaa	cct	gta	aaa	cca	gaa	aac	tca	acg	gat	2304
Pro	Glu	Ala	Pro	Asn	Glu	Lys	Pro	Val	Lys	Pro	Glu	Asn	Ser	Thr	Asp	
		755					760					765				
aat	gga	atg	ttg	aat	cca	gaa	ggg	aat	gtg	ggg	agt	gac	cct	atg	tta	2352
Asn	Gly	Met	Leu	Asn	Pro	Glu	Gly	Asn	Val	Gly	Ser	Asp	Pro	Met	Leu	
		770				775					780					
gat	tca	gca	tta	gag	gaa	gct	cca	gca	gta	gat	cct	gta	caa	gaa	aaa	2400
Asp	Ser	Ala	Leu	Glu	Glu	Ala	Pro	Ala	Val	Asp	Pro	Val	Gln	Glu	Lys	
785					790					795					800	
tta	gaa	aaa	ttt	aca	gct	agt	tac	gga	tta	ggc	tta	gat	agt	gtt	ata	2448
Leu	Glu	Lys	Phe	Thr	Ala	Ser	Tyr	Gly	Leu	Gly	Leu	Asp	Ser	Val	Ile	
				805					810					815		

ttc aat atg gat gga acg att gaa tta aga ttg cca agt gga gaa gtg 2496
 Phe Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val
 820 825 830

ata aaa aag aat tta ttg atc tca tagcgtaa 2528
 Ile Lys Lys Asn Leu Leu Ile Ser
 835 840

<210> 16
 <211> 840
 <212> PRT
 <213> S. pneumoniae

<400> 16
 Cys Ala Tyr Ala Leu Asn Gln His Arg Ser Gln Glu Asn Lys Asp Asn
 1 5 10 15
 Asn Arg Val Ser Tyr Val Asp Gly Ser Gln Ser Ser Gln Lys Ser Glu
 20 25 30
 Asn Leu Thr Pro Asp Gln Val Ser Gln Lys Glu Gly Ile Gln Ala Glu
 35 40 45
 Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly
 50 55 60
 Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Leu Phe
 65 70 75 80
 Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp Ala
 85 90 95
 Asp Ile Val Asn Glu Val Lys Gly Gly Tyr Ile Ile Lys Val Asp Gly
 100 105 110
 Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg
 115 120 125
 Thr Lys Asp Glu Ile Asn Arg Gln Lys Gln Glu His Val Lys Asp Asn
 130 135 140
 Glu Lys Val Asn Ser Asn Val Ala Val Ala Arg Ser Gln Gly Arg Tyr
 145 150 155 160
 Thr Thr Asn Asp Gly Tyr Val Phe Asn Pro Ala Asp Ile Ile Glu Asp
 165 170 175
 Thr Gly Asn Ala Tyr Ile Val Pro His Gly Gly His Tyr His Tyr Ile
 180 185 190
 Pro Lys Ser Asp Leu Ser Ala Ser Glu Leu Ala Ala Ala Lys Ala His
 195 200 205
 Leu Ala Gly Lys Asn Met Gln Pro Ser Gln Leu Ser Tyr Ser Ser Thr
 210 215 220
 Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His
 225 230 235 240
 Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp
 245 250 255
 Glu Ser Gly Phe Val Met Ser His Gly Asp His Asn His Tyr Phe Phe
 260 265 270
 Lys Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu
 275 280 285
 Glu Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His
 290 295 300
 Glu Gln Asp Tyr Pro Ser Asn Ala Lys Glu Met Lys Asp Leu Asp Lys
 305 310 315 320
 Lys Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys
 325 330 335

Arg Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro
 340 345 350
 His Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro Val
 355 360 365
 Gly Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu
 370 375 380
 Gly Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu
 385 390 395 400
 Thr Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn
 405 410 415
 Phe Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro
 420 425 430
 Glu Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr
 435 440 445
 Pro Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu
 450 455 460
 Gly Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro
 465 470 475 480
 Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val
 485 490 495
 Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met
 500 505 510
 Ala Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu
 515 520 525
 Arg Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val
 530 535 540
 Arg Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr
 545 550 555 560
 Lys Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr
 565 570 575
 Thr Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala
 580 585 590
 Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu
 595 600 605
 Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg
 610 615 620
 Asn Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro
 625 630 635 640
 Lys Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn
 645 650 655
 Ser Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val
 660 665 670
 Gln Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu
 675 680 685
 Asn Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser
 690 695 700
 Gly Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro
 705 710 715 720
 Gln Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr
 725 730 735
 Gly Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu
 740 745 750
 Pro Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp
 755 760 765
 Asn Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu
 770 775 780

Asp Ser Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys
 785 790 795 800
 Leu Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile
 805 810 815
 Phe Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val
 820 825 830
 Ile Lys Lys Asn Leu Leu Ile Ser
 835 840

<210> 17
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR oligonucleotide primer

<400> 17
 cagtagatct gtgcctatgc actaaac

27

<210> 18
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR oligonucleotide primer

<400> 18
 gatctctaga ctactgctat tccttacgct atg

33

<210> 19
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR oligonucleotide primer

<400> 19
 atcactcgag cattacctgg ataatcctgt

30

<210> 20
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR oligonucleotide primer

<400> 20
 ctgctaagct tatgaaagat ttagat

26

<210> 21
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR oligonucleotide primer

 <400> 21
 gataactcgag ctgctattcc ttac 24

 <210> 22
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR oligonucleotide primer

 <400> 22
 gaatctcgag ttaagctgct gctaattc 28

 <210> 23
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR oligonucleotide primer

 <400> 23
 gacgctcgag cgctatgaaa tcagataaat tc 32

 <210> 24
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR oligonucleotide primer

 <400> 24
 gacgctcgag ggccattacct ggataatcct gttcatg 37

 <210> 25
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR oligonucleotide primer

 <400> 25
 cagtagatct cttcatcatt tattgaaaag agg 33

 <210> 26
 <211> 40
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> PCR oligonucleotide primer

<400> 26

ttattttcttc catatggact tgacagaaga gcaaattaag

40

<210> 27

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR oligonucleotide primer

<400> 27

cgccaagctt cgctatgaaa tcagataaat tc

32

<210> 28

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR oligonucleotide primer

<400> 28

cgccaagctt ttccacaata taagtcgatt gatt

34

<210> 29

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR oligonucleotide primer

<400> 29

ttattttcttc catatggaag tacctatctt ggaaaaagaa

40

<210> 30

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR oligonucleotide primer

<400> 30

ttattttcttc catatggtgc ctatgcacta aaccagc

37

<210> 31

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR oligonucleotide primer

<400> 31
 ataagaatgc ggccgcttcc acaatataag tcgattgatt 40

 <210> 32
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR oligonucleotide primer

 <400> 32
 cagtagatct gtgcttatga actaggtttg c 31

 <210> 33
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR oligonucleotide primer

 <400> 33
 gatcaagctt gctgctacct ttacttactc tc 32

 <210> 34
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR oligonucleotide primer

 <400> 34
 ctgagatatc cgttatcggtt caaacc 26

 <210> 35
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR oligonucleotide primer

 <400> 35
 ctgcaagctt ttaaaggga ataatacg 28

 <210> 36
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR oligonucleotide primer

 <400> 36
 cagtagatct gcagaagcct tcctatctg 29

<210> 37
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR oligonucleotide primer

<400> 37
 tcgccaaagct tcgttatcgt tcaaaccatt ggg 33

<210> 38
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR oligonucleotide primer

<400> 38
 ataagaatgc ggccgcctta ctctccttta ataaagccaa tagtt 45

<210> 39
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR oligonucleotide primer

<400> 39
 catgccatgg acattgatag tctcttgaaa cagc 34

<210> 40
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR oligonucleotide primer

<400> 40
 cgccaagctt ctactctcc tttaataaag ccaatag 37

<210> 41
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR oligonucleotide primer

<400> 41
 cgacaagctt aacatggctg ctagcgttac c 31

<210> 42

<211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR oligonucleotide primer

<400> 42
 cataccatgg gcctttatga ggcacctaag 30

<210> 43
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR oligonucleotide primer

<400> 43
 cgacaagctt aagtaaactc tcagcctctc tcag 34

<210> 44
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR oligonucleotide primer

<400> 44
 gataccatgg ctacgcacca tgttcaaaga a 31

<210> 45
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR oligonucleotide primer

<400> 45
 cgccaagctt atcatccact aacttgactt tatcac 36

<210> 46
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR oligonucleotide primer

<400> 46
 cataccatgg atattcttgc cttcttagct ccg 33

<210> 47
 <211> 30
 <212> DNA

<213> Artificial Sequence

<220>

<223> PCR oligonucleotide primer

<400> 47

catgccatgg tgcttatgaa ctaggtttgc

30

<210> 48

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR oligonucleotide primer

<400> 48

cgccaagctt tagcgttacc aaaaccatta tc

32

<210> 49

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR oligonucleotide primer

<400> 49

gtattagatc tgttcctatg aacttggtcg tcacca

36

<210> 50

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR oligonucleotide primer

<400> 50

cgcctctaga ctactgtata ggagccgg

28

<210> 51

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR oligonucleotide primer

<400> 51

catgccatgg aaaacatttc aagcctttta cgtg

34

<210> 52

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR oligonucleotide primer

<400> 52

cgacaagctt ctgtatagga gccggttgac tttc

34

<210> 53

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR oligonucleotide primer

<400> 53

catgccatgg ttcgtaaaaa taaggcagac caag

34

<210> 54

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR oligonucleotide primer

<400> 54

catgccatgg aagcctattg gaatgggaag

30

<210> 55

<211> 1019

<212> PRT

<213> S. pneumoniae

<400> 55

Cys Ala Tyr Ala Leu Asn Gln His Arg Ser Gln Glu Asn Lys Asp Asn
 1 5 10 15
 Asn Arg Val Ser Tyr Val Asp Gly Ser Gln Ser Ser Gln Lys Ser Glu
 20 25 30
 Asn Leu Thr Pro Asp Gln Val Ser Gln Lys Glu Gly Ile Gln Ala Glu
 35 40 45
 Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly
 50 55 60
 Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Leu Phe
 65 70 75 80
 Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp Ala
 85 90 95
 Asp Ile Val Asn Glu Val Lys Gly Gly Tyr Ile Ile Lys Val Asp Gly
 100 105 110
 Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg
 115 120 125
 Thr Lys Asp Glu Ile Asn Arg Gln Lys Gln Glu His Val Lys Asp Asn
 130 135 140
 Glu Lys Val Asn Ser Asn Val Ala Val Ala Arg Ser Gln Gly Arg Tyr
 145 150 155 160
 Thr Thr Asn Asp Gly Tyr Val Phe Asn Pro Ala Asp Ile Ile Glu Asp
 165 170 175

Thr Gly Asn Ala Tyr Ile Val Pro His Gly Gly His Tyr His Tyr Ile
 180 185 190
 Pro Lys Ser Asp Leu Ser Ala Ser Glu Leu Ala Ala Ala Lys Ala His
 195 200 205
 Leu Ala Gly Lys Asn Met Gln Pro Ser Gln Leu Ser Tyr Ser Ser Thr
 210 215 220
 Ala Ser Asp Asn Asn Thr Gln Ser Val Ala Lys Gly Ser Thr Ser Lys
 225 230 235 240
 Pro Ala Asn Lys Ser Glu Asn Leu Gln Ser Leu Leu Lys Glu Leu Tyr
 245 250 255
 Asp Ser Pro Ser Ala Gln Arg Tyr Ser Glu Ser Asp Gly Leu Val Phe
 260 265 270
 Asp Pro Ala Lys Ile Ile Ser Arg Thr Pro Asn Gly Val Ala Ile Pro
 275 280 285
 His Gly Asp His Tyr His Phe Ile Pro Tyr Ser Lys Leu Ser Ala Leu
 290 295 300
 Glu Glu Lys Ile Ala Arg Met Val Pro Ile Ser Gly Thr Gly Ser Thr
 305 310 315 320
 Val Ser Thr Asn Ala Lys Pro Asn Glu Val Val Ser Ser Leu Gly Ser
 325 330 335
 Leu Ser Ser Asn Pro Ser Ser Leu Thr Thr Ser Lys Glu Leu Ser Ser
 340 345 350
 Ala Ser Asp Gly Tyr Ile Phe Asn Pro Lys Asp Ile Val Glu Glu Thr
 355 360 365
 Ala Thr Ala Tyr Ile Val Arg His Gly Asp His Phe His Tyr Ile Pro
 370 375 380
 Lys Ser Asn Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala
 385 390 395 400
 Thr Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys
 405 410 415
 His Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu
 420 425 430
 Asp Glu Ser Gly Phe Val Met Ser His Gly Asp His Asn His Tyr Phe
 435 440 445
 Phe Lys Lys Asp Leu Thr Glu Gln Ile Lys Ala Ala Gln Lys His
 450 455 460
 Leu Glu Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser
 465 470 475 480
 His Glu Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp
 485 490 495
 Lys Lys Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val
 500 505 510
 Lys Arg Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr
 515 520 525
 Pro His Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro
 530 535 540
 Val Gly Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu
 545 550 555 560
 Glu Gly Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu
 565 570 575
 Leu Thr Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln
 580 585 590
 Asn Phe Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro
 595 600 605
 Pro Glu Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile
 610 615 620

Thr Pro Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly
 625 630 635 640
 Glu Gly Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu
 645 650 655
 Pro Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu
 660 665 670
 Val Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys
 675 680 685
 Met Ala Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr
 690 695 700
 Leu Arg Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu
 705 710 715 720
 Val Arg Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn
 725 730 735
 Tyr Lys Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly
 740 745 750
 Thr Thr Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn
 755 760 765
 Ala Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu
 770 775 780
 Glu Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys
 785 790 795 800
 Arg Asn Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu
 805 810 815
 Pro Lys Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly
 820 825 830
 Asn Ser Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro
 835 840 845
 Val Gln Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu
 850 855 860
 Glu Asn Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro
 865 870 875 880
 Ser Gly Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala
 885 890 895
 Pro Gln Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser
 900 905 910
 Thr Gly Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser
 915 920 925
 Leu Pro Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr
 930 935 940
 Asp Asn Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met
 945 950 955 960
 Leu Asp Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu
 965 970 975
 Lys Leu Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val
 980 985 990
 Ile Phe Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu
 995 1000 1005
 Val Ile Lys Lys Asn Leu Ser Asp Phe Ile Ala
 1010 1015

<210> 56
 <211> 489
 <212> PRT
 <213> S. pneumoniae

<400> 56
 Cys Ala Tyr Ala Leu Asn Gln His Arg Ser Gln Glu Asn Lys Asp Asn
 1 5 10 15
 Asn Arg Val Ser Tyr Val Asp Gly Ser Gln Ser Ser Gln Lys Ser Glu
 20 25 30
 Asn Leu Thr Pro Asp Gln Val Ser Gln Lys Glu Gly Ile Gln Ala Glu
 35 40 45
 Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly
 50 55 60
 Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Leu Phe
 65 70 75 80
 Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp Ala
 85 90 95
 Asp Ile Val Asn Glu Val Lys Gly Gly Tyr Ile Ile Lys Val Asp Gly
 100 105 110
 Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg
 115 120 125
 Thr Lys Asp Glu Ile Asn Arg Gln Lys Glu His Val Lys Asp Asn
 130 135 140
 Glu Lys Val Asn Ser Asn Val Ala Val Ala Arg Ser Gln Gly Arg Tyr
 145 150 155 160
 Thr Thr Asn Asp Gly Tyr Val Phe Asn Pro Ala Asp Ile Ile Glu Asp
 165 170 175
 Thr Gly Asn Ala Tyr Ile Val Pro His Gly Gly His Tyr His Tyr Ile
 180 185 190
 Pro Lys Ser Asp Leu Ser Ala Ser Glu Leu Ala Ala Ala Lys Ala His
 195 200 205
 Leu Ala Gly Lys Asn Met Gln Pro Ser Gln Leu Ser Tyr Ser Ser Thr
 210 215 220
 Ala Ser Asp Asn Asn Thr Gln Ser Val Ala Lys Gly Ser Thr Ser Lys
 225 230 235 240
 Pro Ala Asn Lys Ser Glu Asn Leu Gln Ser Leu Leu Lys Glu Leu Tyr
 245 250 255
 Asp Ser Pro Ser Ala Gln Arg Tyr Ser Glu Ser Asp Gly Leu Val Phe
 260 265 270
 Asp Pro Ala Lys Ile Ile Ser Arg Thr Pro Asn Gly Val Ala Ile Pro
 275 280 285
 His Gly Asp His Tyr His Phe Ile Pro Tyr Ser Lys Leu Ser Ala Leu
 290 295 300
 Glu Glu Lys Ile Ala Arg Met Val Pro Ile Ser Gly Thr Gly Ser Thr
 305 310 315 320
 Val Ser Thr Asn Ala Lys Pro Asn Glu Val Val Ser Ser Leu Gly Ser
 325 330 335
 Leu Ser Ser Asn Pro Ser Ser Leu Thr Thr Ser Lys Glu Leu Ser Ser
 340 345 350
 Ala Ser Asp Gly Tyr Ile Phe Asn Pro Lys Asp Ile Val Glu Glu Thr
 355 360 365
 Ala Thr Ala Tyr Ile Val Arg His Gly Asp His Phe His Tyr Ile Pro
 370 375 380
 Lys Ser Asn Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala
 385 390 395 400
 Thr Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys
 405 410 415
 His Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu
 420 425 430
 Asp Glu Ser Gly Phe Val Met Ser His Gly Asp His Asn His Tyr Phe
 435 440 445

Phe Lys Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His
 450 455 460
 Leu Glu Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser
 465 470 475 480
 His Glu Gln Asp Tyr Pro Gly Asn Ala
 485

<210> 57
 <211> 509
 <212> PRT
 <213> S. pneumoniae

<400> 57

Met Lys Phe Ser Lys Lys Tyr Ile Ala Ala Gly Ser Ala Val Ile Val
 1 5 10 15
 Ser Leu Ser Leu Cys Ala Tyr Ala Leu Asn Gln His Arg Ser Gln Glu
 20 25 30
 Asn Lys Asp Asn Asn Arg Val Ser Tyr Val Asp Gly Ser Gln Ser Ser
 35 40 45
 Gln Lys Ser Glu Asn Leu Thr Pro Asp Gln Val Ser Gln Lys Glu Gly
 50 55 60
 Ile Gln Ala Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val
 65 70 75 80
 Thr Ser His Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr
 85 90 95
 Asp Ala Leu Phe Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln
 100 105 110
 Leu Lys Asp Ala Asp Ile Val Asn Glu Val Lys Gly Gly Tyr Ile Ile
 115 120 125
 Lys Val Asp Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala
 130 135 140
 Asp Asn Val Arg Thr Lys Asp Glu Ile Asn Arg Gln Lys Gln Glu His
 145 150 155 160
 Val Lys Asp Asn Glu Lys Val Asn Ser Asn Val Ala Val Ala Arg Ser
 165 170 175
 Gln Gly Arg Tyr Thr Thr Asn Asp Gly Tyr Val Phe Asn Pro Ala Asp
 180 185 190
 Ile Ile Glu Asp Thr Gly Asn Ala Tyr Ile Val Pro His Gly Gly His
 195 200 205
 Tyr His Tyr Ile Pro Lys Ser Asp Leu Ser Ala Ser Glu Leu Ala Ala
 210 215 220
 Ala Lys Ala His Leu Ala Gly Lys Asn Met Gln Pro Ser Gln Leu Ser
 225 230 235 240
 Tyr Ser Ser Thr Ala Ser Asp Asn Asn Thr Gln Ser Val Ala Lys Gly
 245 250 255
 Ser Thr Ser Lys Pro Ala Asn Lys Ser Glu Asn Leu Gln Ser Leu Leu
 260 265 270
 Lys Glu Leu Tyr Asp Ser Pro Ser Ala Gln Arg Tyr Ser Glu Ser Asp
 275 280 285
 Gly Leu Val Phe Asp Pro Ala Lys Ile Ile Ser Arg Thr Pro Asn Gly
 290 295 300
 Val Ala Ile Pro His Gly Asp His Tyr His Phe Ile Pro Tyr Ser Lys
 305 310 315 320
 Leu Ser Ala Leu Glu Lys Ile Ala Arg Met Val Pro Ile Ser Gly
 325 330 335
 Thr Gly Ser Thr Val Ser Thr Asn Ala Lys Pro Asn Glu Val Val Ser
 340 345 350

Ser Leu Gly Ser Leu Ser Ser Asn Pro Ser Ser Leu Thr Thr Ser Lys
 355 360 365
 Glu Leu Ser Ser Ala Ser Asp Gly Tyr Ile Phe Asn Pro Lys Asp Ile
 370 375 380
 Val Glu Glu Thr Ala Thr Ala Tyr Ile Val Arg His Gly Asp His Phe
 385 390 395 400
 His Tyr Ile Pro Lys Ser Asn Gln Ile Gly Gln Pro Thr Leu Pro Asn
 405 410 415
 Asn Ser Leu Ala Thr Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr
 420 425 430
 Ser His Glu Lys His Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg
 435 440 445
 Ile Ile Ala Glu Asp Glu Ser Gly Phe Val Met Ser His Gly Asp His
 450 455 460
 Asn His Tyr Phe Phe Lys Lys Asp Leu Thr Glu Glu Ile Lys Ala
 465 470 475 480
 Ala Gln Lys His Leu Glu Glu Val Lys Thr Ser His Asn Gly Leu Asp
 485 490 495
 Ser Leu Ser Ser His Glu Gln Asp Tyr Pro Gly Asn Ala
 500 505

<210> 58
 <211> 1057
 <212> PRT
 <213> S. pneumoniae

<400> 58

Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu Glu
 1 5 10 15
 Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu Gln
 20 25 30
 Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys Ile
 35 40 45
 Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg Glu
 50 55 60
 Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro His Gly
 65 70 75 80
 Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly Ile
 85 90 95
 Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly Val
 100 105 110
 Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr Asn
 115 120 125
 Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe Thr
 130 135 140
 Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu Leu
 145 150 155 160
 Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro Asp
 165 170 175
 Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly Val
 180 185 190
 Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly Gln
 195 200 205
 Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser Tyr
 210 215 220
 Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala Ser
 225 230 235 240

Gln	Thr	Ile	Phe	Tyr	Pro	Phe	His	Ala	Gly	Asp	Thr	Tyr	Leu	Arg	Val	245	250	255
Asn	Pro	Gln	Phe	Ala	Val	Pro	Lys	Gly	Thr	Asp	Ala	Leu	Val	Arg	Val	260	265	270
Phe	Asp	Glu	Phe	His	Gly	Asn	Ala	Tyr	Leu	Glu	Asn	Asn	Tyr	Lys	Val	275	280	285
Gly	Glu	Ile	Lys	Leu	Pro	Ile	Pro	Lys	Leu	Asn	Gln	Gly	Thr	Thr	Arg	290	295	300
Thr	Ala	Gly	Asn	Lys	Ile	Pro	Val	Thr	Phe	Met	Ala	Asn	Ala	Tyr	Leu	305	310	315
Asp	Asn	Gln	Ser	Thr	Tyr	Ile	Val	Glu	Val	Pro	Ile	Leu	Glu	Lys	Glu	325	330	335
Asn	Gln	Thr	Asp	Lys	Pro	Ser	Ile	Leu	Pro	Gln	Phe	Lys	Arg	Asn	Lys	340	345	350
Ala	Gln	Glu	Asn	Ser	Lys	Leu	Asp	Glu	Lys	Val	Glu	Glu	Pro	Lys	Thr	355	360	365
Ser	Glu	Lys	Val	Glu	Lys	Glu	Lys	Leu	Ser	Glu	Thr	Gly	Asn	Ser	Thr	370	375	380
Ser	Asn	Ser	Thr	Leu	Glu	Glu	Val	Pro	Thr	Val	Asp	Pro	Val	Gln	Glu	385	390	395
Lys	Val	Ala	Lys	Phe	Ala	Glu	Ser	Tyr	Gly	Met	Lys	Leu	Glu	Asn	Val	405	410	415
Leu	Phe	Asn	Met	Asp	Gly	Thr	Ile	Glu	Leu	Tyr	Leu	Pro	Ser	Gly	Glu	420	425	430
Val	Ile	Lys	Lys	Asn	Met	Ala	Asp	Phe	Thr	Gly	Glu	Ala	Pro	Gln	Gly	435	440	445
Asn	Gly	Glu	Asn	Lys	Pro	Ser	Glu	Asn	Gly	Lys	Val	Ser	Thr	Gly	Thr	450	455	460
Val	Glu	Asn	Gln	Pro	Thr	Glu	Asn	Lys	Pro	Ala	Asp	Ser	Leu	Pro	Glu	465	470	475
Ala	Pro	Asn	Glu	Lys	Pro	Val	Lys	Pro	Glu	Asn	Ser	Thr	Asp	Asn	Gly	485	490	495
Met	Leu	Asn	Pro	Glu	Gly	Asn	Val	Gly	Ser	Asp	Pro	Met	Leu	Asp	Pro	500	505	510
Ala	Leu	Glu	Ala	Pro	Ala	Val	Asp	Pro	Val	Gln	Glu	Lys	Leu	Glu		515	520	525
Lys	Phe	Thr	Ala	Ser	Tyr	Gly	Leu	Gly	Leu	Asp	Ser	Val	Ile	Phe	Asn	530	535	540
Met	Asp	Gly	Thr	Ile	Glu	Leu	Arg	Leu	Pro	Ser	Gly	Glu	Val	Ile	Lys	545	550	555
Lys	Asn	Leu	Ser	Asp	Phe	Ile	Ala	Lys	Leu	Arg	Tyr	Arg	Ser	Asn	His	565	570	575
Trp	Val	Pro	Asp	Ser	Arg	Pro	Glu	Glu	Pro	Ser	Pro	Gln	Pro	Thr	Pro	580	585	590
Glu	Pro	Ser	Pro	Ser	Pro	Gln	Pro	Ala	Pro	Asn	Pro	Gln	Pro	Ala	Pro	595	600	605
Ser	Asn	Pro	Ile	Asp	Glu	Lys	Leu	Val	Lys	Glu	Ala	Val	Arg	Lys	Val	610	615	620
Gly	Asp	Gly	Tyr	Val	Phe	Glu	Glu	Asn	Gly	Val	Ser	Arg	Tyr	Ile	Pro	625	630	635
Ala	Lys	Asn	Leu	Ser	Ala	Glu	Thr	Ala	Ala	Gly	Ile	Asp	Ser	Lys	Leu	645	650	655
Ala	Lys	Gln	Glu	Ser	Leu	Ser	His	Lys	Leu	Gly	Ala	Lys	Lys	Thr	Asp	660	665	670
Leu	Pro	Ser	Ser	Asp	Arg	Glu	Phe	Tyr	Asn	Lys	Ala	Tyr	Asp	Leu	Leu	675	680	685

Ala Arg Ile His Gln Asp Leu Leu Asp Asn Lys Gly Arg Gln Val Asp
690 695 700
Phe Glu Ala Leu Asp Asn Leu Leu Glu Arg Leu Lys Asp Val Ser Ser
705 710 715 720
Asp Lys Val Lys Leu Val Asp Asp Ile Leu Ala Phe Leu Ala Pro Ile
725 730 735
Arg His Pro Glu Arg Leu Gly Lys Pro Asn Ala Gln Ile Thr Tyr Thr
740 745 750
Asp Asp Glu Ile Gln Val Ala Lys Leu Ala Gly Lys Tyr Thr Thr Glu
755 760 765
Asp Gly Tyr Ile Phe Asp Pro Arg Asp Ile Thr Ser Asp Glu Gly Asp
770 775 780
Ala Tyr Val Thr Pro His Met Thr His Ser His Trp Ile Lys Lys Asp
785 790 795 800
Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr Ala Lys Glu
805 810 815
Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser Gly Asn Thr
820 825 830
Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys Ala Ala Lys
835 840 845
Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr Thr Val Glu
850 855 860
Val Lys Asn Gly Ser Leu Ile Ile Pro His Tyr Asp His Tyr His Asn
865 870 875 880
Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala Pro Lys Gly
885 890 895
Tyr Thr Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr Val Glu His
900 905 910
Pro Asn Glu Arg Pro His Ser Asp Asn Gly Phe Gly Asn Ala Ser Asp
915 920 925
His Val Gln Arg Asn Lys Asn Gly Gln Ala Asp Thr Asn Gln Thr Glu
930 935 940
Lys Pro Ser Glu Glu Lys Pro Gln Thr Glu Lys Pro Glu Glu Glu Thr
945 950 955 960
Pro Arg Glu Glu Lys Pro Gln Ser Glu Lys Pro Glu Ser Pro Lys Pro
965 970 975
Thr Glu Glu Pro Glu Glu Glu Ser Pro Glu Glu Ser Glu Glu Pro Gln
980 985 990
Val Glu Thr Glu Lys Val Glu Glu Lys Leu Arg Glu Ala Glu Asp Leu
995 1000 1005
Leu Gly Lys Ile Gln Asp Pro Ile Ile Lys Ser Asn Ala Lys Glu Thr
1010 1015 1020
Leu Thr Gly Leu Lys Asn Asn Leu Leu Phe Gly Thr Gln Asp Asn Asn
1025 1030 1035 1040
Thr Ile Met Ala Glu Ala Glu Lys Leu Leu Ala Leu Leu Lys Glu Ser
1045 1050 1055
Lys

<210> 59
<211> 205
<212> PRT
<213> S. pneumoniae

<400> 59
Cys Ala Tyr Ala Leu Asn Gln His Arg Ser Gln Glu Asn Lys Asp Asn
1 5 10 15

Asn Arg Val Ser Tyr Val Asp Gly Ser Gln Ser Ser Gln Lys Ser Glu
 20 25 30
 Asn Leu Thr Pro Asp Gln Val Ser Gln Lys Glu Gly Ile Gln Ala Glu
 35 40 45
 Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly
 50 55 60
 Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Leu Phe
 65 70 75 80
 Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp Ala
 85 90 95
 Asp Ile Val Asn Glu Val Lys Gly Gly Tyr Ile Ile Lys Val Asp Gly
 100 105 110
 Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg
 115 120 125
 Thr Lys Asp Glu Ile Asn Arg Gln Lys Gln Glu His Val Lys Asp Asn
 130 135 140
 Glu Lys Val Asn Ser Asn Val Ala Val Ala Arg Ser Gln Gly Arg Tyr
 145 150 155 160
 Thr Thr Asn Asp Gly Tyr Val Phe Asn Pro Ala Asp Ile Ile Glu Asp
 165 170 175
 Thr Gly Asn Ala Tyr Ile Val Pro His Gly Gly His Tyr His Tyr Ile
 180 185 190
 Pro Lys Ser Asp Leu Ser Ala Ser Glu Leu Ala Ala Ala
 195 200 205

<210> 60
 <211> 821
 <212> PRT
 <213> S. pneumoniae

<400> 60
 Cys Ala Tyr Glu Leu Gly Leu His Gln Ala Gln Thr Val Lys Glu Asn
 1 5 10 15
 Asn Arg Val Ser Tyr Ile Asp Gly Lys Gln Ala Thr Gln Lys Thr Glu
 20 25 30
 Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala Glu
 35 40 45
 Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly
 50 55 60
 Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile Ile
 65 70 75 80
 Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp Ser
 85 90 95
 Asp Ile Val Asn Glu Ile Lys Gly Gly Tyr Val Ile Lys Val Asn Gly
 100 105 110
 Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg
 115 120 125
 Thr Lys Glu Glu Ile Asn Arg Gln Lys Gln Glu His Ser Gln His Arg
 130 135 140
 Glu Gly Gly Thr Ser Ala Asn Asp Gly Ala Val Ala Phe Ala Arg Ser
 145 150 155 160
 Gln Gly Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser Asp
 165 170 175
 Ile Ile Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asp His
 180 185 190
 Tyr His Tyr Ile Pro Lys Asn Glu Leu Ser Ala Ser Glu Leu Ala Ala
 195 200 205

Ala Glu Ala Phe Leu Ser Gly Arg Glu Asn Leu Ser Asn Leu Arg Thr
 210 215 220
 Tyr Arg Arg Gln Asn Ser Asp Asn Thr Pro Arg Thr Asn Trp Val Pro
 225 230 235 240
 Ser Val Ser Asn Pro Gly Thr Thr Asn Thr Asn Thr Ser Asn Asn Ser
 245 250 255
 Asn Thr Asn Ser Gln Ala Ser Gln Ser Asn Asp Ile Asp Ser Leu Leu
 260 265 270
 Lys Gln Leu Tyr Lys Leu Pro Leu Ser Gln Arg His Val Glu Ser Asp
 275 280 285
 Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr Ala Arg Gly
 290 295 300
 Val Ala Val Pro His Gly Asn His Tyr His Phe Ile Pro Tyr Glu Gln
 305 310 315 320
 Met Ser Glu Leu Glu Lys Arg Ile Ala Arg Ile Ile Pro Leu Arg Tyr
 325 330 335
 Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Glu Pro Ser Pro
 340 345 350
 Gln Pro Thr Pro Glu Pro Ser Pro Ser Pro Gln Pro Ala Pro Asn Pro
 355 360 365
 Gln Pro Ala Pro Ser Asn Pro Ile Asp Glu Lys Leu Val Lys Glu Ala
 370 375 380
 Val Arg Lys Val Gly Asp Gly Tyr Val Phe Glu Glu Asn Gly Val Ser
 385 390 395 400
 Arg Tyr Ile Pro Ala Lys Asn Leu Ser Ala Glu Thr Ala Ala Gly Ile
 405 410 415
 Asp Ser Lys Leu Ala Lys Gln Glu Ser Leu Ser His Lys Leu Gly Ala
 420 425 430
 Lys Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu Phe Tyr Asn Lys Ala
 435 440 445
 Tyr Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp Asn Lys Gly
 450 455 460
 Arg Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu Arg Leu Lys
 465 470 475 480
 Asp Val Ser Ser Asp Lys Val Lys Leu Val Asp Asp Ile Leu Ala Phe
 485 490 495
 Leu Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro Asn Ala Gln
 500 505 510
 Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala Gly Lys
 515 520 525
 Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp Ile Thr Ser
 530 535 540
 Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His Ser His Trp
 545 550 555 560
 Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala
 565 570 575
 Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp
 580 585 590
 Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val
 595 600 605
 Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln
 610 615 620
 Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His Tyr Asp
 625 630 635 640
 His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu
 645 650 655

Ala Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr
660 665 670
Tyr Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn Gly Phe Gly
675 680 685
Asn Ala Ser Asp His Val Gln Arg Asn Lys Asn Gly Gln Ala Asp Thr
690 695 700
Asn Gln Thr Glu Lys Pro Ser Glu Glu Lys Pro Gln Thr Glu Lys Pro
705 710 715 720
Glu Glu Glu Thr Pro Arg Glu Glu Lys Pro Gln Ser Glu Lys Pro Glu
725 730 735
Ser Pro Lys Pro Thr Glu Glu Pro Glu Glu Glu Ser Pro Glu Glu Ser
740 745 750
Glu Glu Pro Gln Val Glu Thr Glu Lys Val Glu Glu Lys Leu Arg Glu
755 760 765
Ala Glu Asp Leu Leu Gly Lys Ile Gln Asp Pro Ile Ile Lys Ser Asn
770 775 780
Ala Lys Glu Thr Leu Thr Gly Leu Lys Asn Asn Leu Leu Phe Gly Thr
785 790 795 800
Gln Asp Asn Asn Thr Ile Met Ala Glu Ala Glu Lys Leu Leu Ala Leu
805 810 815
Leu Lys Glu Ser Lys
820

<210> 61
<211> 334
<212> PRT
<213> S. pneumoniae

<400> 61

Cys Ala Tyr Glu Leu Gly Leu His Gln Ala Gln Thr Val Lys Glu Asn
1 5 10 15
Asn Arg Val Ser Tyr Ile Asp Gly Lys Gln Ala Thr Gln Lys Thr Glu
20 25 30
Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala Glu
35 40 45
Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly
50 55 60
Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile Ile
65 70 75 80
Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp Ser
85 90 95
Asp Ile Val Asn Glu Ile Lys Gly Gly Tyr Val Ile Lys Val Asn Gly
100 105 110
Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg
115 120 125
Thr Lys Glu Glu Ile Asn Arg Gln Lys Gln Glu His Ser Gln His Arg
130 135 140
Glu Gly Gly Thr Ser Ala Asn Asp Gly Ala Val Ala Phe Ala Arg Ser
145 150 155 160
Gln Gly Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser Asp
165 170 175
Ile Ile Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asp His
180 185 190
Tyr His Tyr Ile Pro Lys Asn Glu Leu Ser Ala Ser Glu Leu Ala Ala
195 200 205
Ala Glu Ala Phe Leu Ser Gly Arg Glu Asn Leu Ser Asn Leu Arg Thr
210 215 220

Tyr Arg Arg Gln Asn Ser Asp Asn Thr Pro Arg Thr Asn Trp Val Pro
 225 230 235 240
 Ser Val Ser Asn Pro Gly Thr Thr Asn Thr Asn Thr Ser Asn Asn Ser
 245 250 255
 Asn Thr Asn Ser Gln Ala Ser Gln Ser Asn Asp Ile Asp Ser Leu Leu
 260 265 270
 Lys Gln Leu Tyr Lys Leu Pro Leu Ser Gln Arg His Val Glu Ser Asp
 275 280 285
 Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr Ala Arg Gly
 290 295 300
 Val Ala Val Pro His Gly Asn His Tyr His Phe Ile Pro Tyr Glu Gln
 305 310 315 320
 Met Ser Glu Leu Glu Lys Arg Ile Ala Arg Ile Ile Pro Leu
 325 330

<210> 62
 <211> 487
 <212> PRT
 <213> S. pneumoniae

<400> 62

Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Glu Pro
 1 5 10 15
 Ser Pro Gln Pro Thr Pro Glu Pro Ser Pro Ser Pro Gln Pro Ala Pro
 20 25 30
 Asn Pro Gln Pro Ala Pro Ser Asn Pro Ile Asp Glu Lys Leu Val Lys
 35 40 45
 Glu Ala Val Arg Lys Val Gly Asp Gly Tyr Val Phe Glu Glu Asn Gly
 50 55 60
 Val Ser Arg Tyr Ile Pro Ala Lys Asn Leu Ser Ala Glu Thr Ala Ala
 65 70 75 80
 Gly Ile Asp Ser Lys Leu Ala Lys Gln Glu Ser Leu Ser His Lys Leu
 85 90 95
 Gly Ala Lys Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu Phe Tyr Asn
 100 105 110
 Lys Ala Tyr Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp Asn
 115 120 125
 Lys Gly Arg Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu Arg
 130 135 140
 Leu Lys Asp Val Ser Ser Asp Lys Val Lys Leu Val Asp Asp Ile Leu
 145 150 155 160
 Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro Asn
 165 170 175
 Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
 180 185 190
 Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp Ile
 195 200 205
 Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His Ser
 210 215 220
 His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala
 225 230 235 240
 Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His
 245 250 255
 Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn
 260 265 270
 Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn
 275 280 285

Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His
 290 295 300
 Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu
 305 310 315 320
 Tyr Glu Ala Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu Ala Thr Val
 325 330 335
 Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn Gly
 340 345 350
 Phe Gly Asn Ala Ser Asp His Val Gln Arg Asn Lys Asn Gly Gln Ala
 355 360 365
 Asp Thr Asn Gln Thr Glu Lys Pro Ser Glu Glu Lys Pro Gln Thr Glu
 370 375 380
 Lys Pro Glu Glu Glu Thr Pro Arg Glu Glu Lys Pro Gln Ser Glu Lys
 385 390 395 400
 Pro Glu Ser Pro Lys Pro Thr Glu Glu Pro Glu Glu Glu Ser Pro Glu
 405 410 415
 Glu Ser Glu Glu Pro Gln Val Glu Thr Glu Lys Val Glu Glu Lys Leu
 420 425 430
 Arg Glu Ala Glu Asp Leu Leu Gly Lys Ile Gln Asp Pro Ile Ile Lys
 435 440 445
 Ser Asn Ala Lys Glu Thr Leu Thr Gly Leu Lys Asn Asn Leu Leu Phe
 450 455 460
 Gly Thr Gln Asp Asn Asn Thr Ile Met Ala Glu Ala Glu Lys Leu Leu
 465 470 475 480
 Ala Leu Leu Lys Glu Ser Lys
 485

<210> 63
 <211> 613
 <212> PRT
 <213> S. pneumoniae

<400> 63

Ala Glu Ala Phe Leu Ser Gly Arg Glu Asn Leu Ser Asn Leu Arg Thr
 1 5 10 15
 Tyr Arg Arg Gln Asn Ser Asp Asn Thr Pro Arg Thr Asn Trp Val Pro
 20 25 30
 Ser Val Ser Asn Pro Gly Thr Thr Asn Thr Asn Thr Ser Asn Asn Ser
 35 40 45
 Asn Thr Asn Ser Gln Ala Ser Gln Ser Asn Asp Ile Asp Ser Leu Leu
 50 55 60
 Lys Gln Leu Tyr Lys Leu Pro Leu Ser Gln Arg His Val Glu Ser Asp
 65 70 75 80
 Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr Ala Arg Gly
 85 90 95
 Val Ala Val Pro His Gly Asn His Tyr His Phe Ile Pro Tyr Glu Gln
 100 105 110
 Met Ser Glu Leu Glu Lys Arg Ile Ala Arg Ile Ile Pro Leu Arg Tyr
 115 120 125
 Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Glu Pro Ser Pro
 130 135 140
 Gln Pro Thr Pro Glu Pro Ser Pro Ser Pro Gln Pro Ala Pro Asn Pro
 145 150 155 160
 Gln Pro Ala Pro Ser Asn Pro Ile Asp Glu Lys Leu Val Lys Glu Ala
 165 170 175
 Val Arg Lys Val Gly Asp Gly Tyr Val Phe Glu Glu Asn Gly Val Ser
 180 185 190

Arg Tyr Ile Pro Ala Lys Asn Leu Ser Ala Glu Thr Ala Ala Gly Ile
 195 200 205
 Asp Ser Lys Leu Ala Lys Gln Glu Ser Leu Ser His Lys Leu Gly Ala
 210 215 220
 Lys Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu Phe Tyr Asn Lys Ala
 225 230 235 240
 Tyr Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp Asn Lys Gly
 245 250 255
 Arg Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu Arg Leu Lys
 260 265 270
 Asp Val Ser Ser Asp Lys Val Lys Leu Val Asp Asp Ile Leu Ala Phe
 275 280 285
 Leu Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro Asn Ala Gln
 290 295 300
 Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala Gly Lys
 305 310 315 320
 Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp Ile Thr Ser
 325 330 335
 Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His Ser His Trp
 340 345 350
 Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala
 355 360 365
 Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp
 370 375 380
 Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val
 385 390 395 400
 Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln
 405 410 415
 Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His Tyr Asp
 420 425 430
 His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu
 435 440 445
 Ala Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr
 450 455 460
 Tyr Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn Gly Phe Gly
 465 470 475 480
 Asn Ala Ser Asp His Val Gln Arg Asn Lys Asn Gly Gln Ala Asp Thr
 485 490 495
 Asn Gln Thr Glu Lys Pro Ser Glu Glu Lys Pro Gln Thr Glu Lys Pro
 500 505 510
 Glu Glu Glu Thr Pro Arg Glu Glu Lys Pro Gln Ser Glu Lys Pro Glu
 515 520 525
 Ser Pro Lys Pro Thr Glu Glu Pro Glu Glu Glu Ser Pro Glu Glu Ser
 530 535 540
 Glu Glu Pro Gln Val Glu Thr Glu Lys Val Glu Glu Lys Leu Arg Glu
 545 550 555 560
 Ala Glu Asp Leu Leu Gly Lys Ile Gln Asp Pro Ile Ile Lys Ser Asn
 565 570 575
 Ala Lys Glu Thr Leu Thr Gly Leu Lys Asn Asn Leu Leu Phe Gly Thr
 580 585 590
 Gln Asp Asn Asn Thr Ile Met Ala Glu Ala Glu Lys Leu Leu Ala Leu
 595 600 605
 Leu Lys Glu Ser Lys
 610


<210> 64

<211> 568

<212> PRT

<213> S. pneumoniae

<400> 64



Asp	Leu	Thr	Glu	Glu	Gln	Ile	Lys	Ala	Ala	Gln	Lys	His	Leu	Glu	Glu
1			5					10					15		
Val	Lys	Thr	Ser	His	Asn	Gly	Leu	Asp	Ser	Leu	Ser	Ser	His	Glu	Gln
			20					25					30		
Asp	Tyr	Pro	Gly	Asn	Ala	Lys	Glu	Met	Lys	Asp	Leu	Asp	Lys	Lys	Ile
			35				40				45				
Glu	Glu	Lys	Ile	Ala	Gly	Ile	Met	Lys	Gln	Tyr	Gly	Val	Lys	Arg	Glu
			50			55				60					
Ser	Ile	Val	Val	Asn	Lys	Glu	Lys	Asn	Ala	Ile	Ile	Tyr	Pro	His	Gly
65				70				75						80	
Asp	His	His	His	Ala	Asp	Pro	Ile	Asp	Glu	His	Lys	Pro	Val	Gly	Ile
				85				90						95	
Gly	His	Ser	His	Ser	Asn	Tyr	Glu	Leu	Phe	Lys	Pro	Glu	Glu	Gly	Val
			100				105					110			
Ala	Lys	Lys	Glu	Gly	Asn	Lys	Val	Tyr	Thr	Gly	Glu	Glu	Leu	Thr	Asn
			115			120					125				
Val	Val	Asn	Leu	Leu	Lys	Asn	Ser	Thr	Phe	Asn	Asn	Gln	Asn	Phe	Thr
			130			135					140				
Leu	Ala	Asn	Gly	Gln	Lys	Arg	Val	Ser	Phe	Ser	Phe	Pro	Pro	Glu	Leu
145				150				155						160	
Glu	Lys	Lys	Leu	Gly	Ile	Asn	Met	Leu	Val	Lys	Leu	Ile	Thr	Pro	Asp
			165			170						175			
Gly	Lys	Val	Leu	Glu	Lys	Val	Ser	Gly	Lys	Val	Phe	Gly	Glu	Gly	Val
			180			185						190			
Gly	Asn	Ile	Ala	Asn	Phe	Glu	Leu	Asp	Gln	Pro	Tyr	Leu	Pro	Gly	Gln
			195			200					205				
Thr	Phe	Lys	Tyr	Thr	Ile	Ala	Ser	Lys	Asp	Tyr	Pro	Glu	Val	Ser	Tyr
			210			215					220				
Asp	Gly	Thr	Phe	Thr	Val	Pro	Thr	Ser	Leu	Ala	Tyr	Lys	Met	Ala	Ser
225				230				235						240	
Gln	Thr	Ile	Phe	Tyr	Pro	Phe	His	Ala	Gly	Asp	Thr	Tyr	Leu	Arg	Val
			245			250							255		
Asn	Pro	Gln	Phe	Ala	Val	Pro	Lys	Gly	Thr	Asp	Ala	Leu	Val	Arg	Val
			260			265						270			
Phe	Asp	Glu	Phe	His	Gly	Asn	Ala	Tyr	Leu	Glu	Asn	Asn	Tyr	Lys	Val
			275			280					285				
Gly	Glu	Ile	Lys	Leu	Pro	Ile	Pro	Lys	Leu	Asn	Gln	Gly	Thr	Thr	Arg
			290			295					300				
Thr	Ala	Gly	Asn	Lys	Ile	Pro	Val	Thr	Phe	Met	Ala	Asn	Ala	Tyr	Leu
305				310				315						320	
Asp	Asn	Gln	Ser	Thr	Tyr	Ile	Val	Glu	Val	Pro	Ile	Leu	Glu	Lys	Glu
			325			330						335			
Asn	Gln	Thr	Asp	Lys	Pro	Ser	Ile	Leu	Pro	Gln	Phe	Lys	Arg	Asn	Lys
			340			345						350			
Ala	Gln	Glu	Asn	Ser	Lys	Leu	Asp	Glu	Lys	Val	Glu	Glu	Pro	Lys	Thr
			355			360					365				
Ser	Glu	Lys	Val	Glu	Lys	Glu	Lys	Leu	Ser	Glu	Thr	Gly	Asn	Ser	Thr
			370			375					380				
Ser	Asn	Ser	Thr	Leu	Glu	Val	Pro	Thr	Val	Asp	Pro	Val	Gln	Glu	
385				390				395						400	
Lys	Val	Ala	Lys	Phe	Ala	Glu	Ser	Tyr	Gly	Met	Lys	Leu	Glu	Asn	Val
			405			410							415		

Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly Glu
 420 425 430
 Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln Gly
 435 440 445
 Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly Thr
 450 455 460
 Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro Glu
 465 470 475 480
 Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn Gly
 485 490 495
 Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp Pro
 500 505 510
 Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu Glu
 515 520 525
 Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe Asn
 530 535 540
 Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile Lys
 545 550 555 560
 Lys Asn Leu Ser Asp Phe Ile Ala
 565

<210> 65
 <211> 329
 <212> PRT
 <213> S. pneumoniae

<400> 65

Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu Glu
 1 5 10 15
 Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu Gln
 20 25 30
 Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys Ile
 35 40 45
 Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg Glu
 50 55 60
 Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro His Gly
 65 70 75 80
 Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly Ile
 85 90 95
 Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly Val
 100 105 110
 Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr Asn
 115 120 125
 Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe Thr
 130 135 140
 Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu Leu
 145 150 155 160
 Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro Asp
 165 170 175
 Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly Val
 180 185 190
 Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly Gln
 195 200 205
 Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser Tyr
 210 215 220
 Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala Ser
 225 230 235 240

Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg Val
 245 250 255
 Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg Val
 260 265 270
 Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys Val
 275 280 285
 Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr Arg
 290 295 300
 Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr Leu
 305 310 315 320
 Asp Asn Gln Ser Thr Tyr Ile Val Glu
 325

<210> 66
 <211> 240
 <212> PRT
 <213> S. pneumoniae

<400> 66

Glu Val Pro Ile Leu Glu Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile
 1 5 10 15
 Leu Pro Gln Phe Lys Arg Asn Lys Ala Gln Glu Asn Ser Lys Leu Asp
 20 25 30
 Glu Lys Val Glu Glu Pro Lys Thr Ser Glu Lys Val Glu Lys Glu Lys
 35 40 45
 Leu Ser Glu Thr Gly Asn Ser Thr Ser Asn Ser Thr Leu Glu Glu Val
 50 55 60
 Pro Thr Val Asp Pro Val Gln Glu Lys Val Ala Lys Phe Ala Glu Ser
 65 70 75 80
 Tyr Gly Met Lys Leu Glu Asn Val Leu Phe Asn Met Asp Gly Thr Ile
 85 90 95
 Glu Leu Tyr Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Met Ala Asp
 100 105 110
 Phe Thr Gly Glu Ala Pro Gln Gly Asn Gly Glu Asn Lys Pro Ser Glu
 115 120 125
 Asn Gly Lys Val Ser Thr Gly Thr Val Glu Asn Gln Pro Thr Glu Asn
 130 135 140
 Lys Pro Ala Asp Ser Leu Pro Glu Ala Pro Asn Glu Lys Pro Val Lys
 145 150 155 160
 Pro Glu Asn Ser Thr Asp Asn Gly Met Leu Asn Pro Glu Gly Asn Val
 165 170 175
 Gly Ser Asp Pro Met Leu Asp Pro Ala Leu Glu Glu Ala Pro Ala Val
 180 185 190
 Asp Pro Val Gln Glu Lys Leu Glu Lys Phe Thr Ala Ser Tyr Gly Leu
 195 200 205
 Gly Leu Asp Ser Val Ile Phe Asn Met Asp Gly Thr Ile Glu Leu Arg
 210 215 220
 Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Leu Ser Asp Phe Ile Ala
 225 230 235 240

<210> 67
 <211> 555
 <212> PRT
 <213> S. pneumoniae

<400> 67

Asp	Ile	Asp	Ser	Leu	Leu	Lys	Gln	Leu	Tyr	Lys	Leu	Pro	Leu	Ser	Gln	1	5	10	15
Arg	His	Val	Glu	Ser	Asp	Gly	Leu	Ile	Phe	Asp	Pro	Ala	Gln	Ile	Thr	20	25	30	
Ser	Arg	Thr	Ala	Arg	Gly	Val	Ala	Val	Pro	His	Gly	Asn	His	Tyr	His	35	40	45	
Phe	Ile	Pro	Tyr	Glu	Gln	Met	Ser	Glu	Leu	Glu	Lys	Arg	Ile	Ala	Arg	50	55	60	
Ile	Ile	Pro	Leu	Arg	Tyr	Arg	Ser	Asn	His	Trp	Val	Pro	Asp	Ser	Arg	65	70	75	80
Pro	Glu	Glu	Pro	Ser	Pro	Gln	Pro	Thr	Pro	Glu	Pro	Ser	Pro	Ser	Pro	85	90	95	
Gln	Pro	Ala	Pro	Asn	Pro	Gln	Pro	Ala	Pro	Ser	Asn	Pro	Ile	Asp	Glu	100	105	110	
Lys	Leu	Val	Lys	Glu	Ala	Val	Arg	Lys	Val	Gly	Asp	Gly	Tyr	Val	Phe	115	120	125	
Glu	Glu	Asn	Gly	Val	Ser	Arg	Tyr	Ile	Pro	Ala	Lys	Asn	Leu	Ser	Ala	130	135	140	
Glu	Thr	Ala	Ala	Gly	Ile	Asp	Ser	Lys	Leu	Ala	Lys	Gln	Glu	Ser	Leu	145	150	155	160
Ser	His	Lys	Leu	Gly	Ala	Lys	Lys	Thr	Asp	Leu	Pro	Ser	Ser	Asp	Arg	165	170	175	
Glu	Phe	Tyr	Asn	Lys	Ala	Tyr	Asp	Leu	Leu	Ala	Arg	Ile	His	Gln	Asp	180	185	190	
Leu	Leu	Asp	Asn	Lys	Gly	Arg	Gln	Val	Asp	Phe	Glu	Ala	Leu	Asp	Asn	195	200	205	
Leu	Leu	Glu	Arg	Leu	Lys	Asp	Val	Ser	Ser	Asp	Lys	Val	Lys	Leu	Val	210	215	220	
Asp	Asp	Ile	Leu	Ala	Phe	Leu	Ala	Pro	Ile	Arg	His	Pro	Glu	Arg	Leu	225	230	235	240
Gly	Lys	Pro	Asn	Ala	Gln	Ile	Thr	Tyr	Thr	Asp	Asp	Glu	Ile	Gln	Val	245	250	255	
Ala	Lys	Leu	Ala	Gly	Lys	Tyr	Thr	Thr	Glu	Asp	Gly	Tyr	Ile	Phe	Asp	260	265	270	
Pro	Arg	Asp	Ile	Thr	Ser	Asp	Glu	Gly	Asp	Ala	Tyr	Val	Thr	Pro	His	275	280	285	
Met	Thr	His	Ser	His	Trp	Ile	Lys	Lys	Asp	Ser	Leu	Ser	Glu	Ala	Glu	290	295	300	
Arg	Ala	Ala	Ala	Gln	Ala	Tyr	Ala	Lys	Glu	Lys	Gly	Leu	Thr	Pro	Pro	305	310	315	320
Ser	Thr	Asp	His	Gln	Asp	Ser	Gly	Asn	Thr	Glu	Ala	Lys	Gly	Ala	Glu	325	330	335	
Ala	Ile	Tyr	Asn	Arg	Val	Lys	Ala	Ala	Lys	Lys	Val	Pro	Leu	Asp	Arg	340	345	350	
Met	Pro	Tyr	Asn	Leu	Gln	Tyr	Thr	Val	Glu	Val	Lys	Asn	Gly	Ser	Leu	355	360	365	
Ile	Ile	Pro	His	Tyr	Asp	His	Tyr	His	Asn	Ile	Lys	Phe	Glu	Trp	Phe	370	375	380	
Asp	Glu	Gly	Leu	Tyr	Glu	Ala	Pro	Lys	Gly	Tyr	Thr	Leu	Glu	Asp	Leu	385	390	395	400
Leu	Ala	Thr	Val	Lys	Tyr	Tyr	Val	Glu	His	Pro	Asn	Glu	Arg	Pro	His	405	410	415	
Ser	Asp	Asn	Gly	Phe	Gly	Asn	Ala	Ser	Asp	His	Val	Gln	Arg	Asn	Lys	420	425	430	
Asn	Gly	Gln	Ala	Asp	Thr	Asn	Gln	Thr	Glu	Lys	Pro	Ser	Glu	Glu	Lys	435	440	445	

Pro Gln Thr Glu Lys Pro Glu Glu Glu Thr Pro Arg Glu Glu Lys Pro
 450 455 460
 Gln Ser Glu Lys Pro Glu Ser Pro Lys Pro Thr Glu Glu Pro Glu Glu
 465 470 475 480
 Glu Ser Pro Glu Glu Ser Glu Glu Pro Gln Val Glu Thr Glu Lys Val
 485 490 495
 Glu Glu Lys Leu Arg Glu Ala Glu Asp Leu Leu Gly Lys Ile Gln Asp
 500 505 510
 Pro Ile Ile Lys Ser Asn Ala Lys Glu Thr Leu Thr Gly Leu Lys Asn
 515 520 525
 Asn Leu Leu Phe Gly Thr Gln Asp Asn Asn Thr Ile Met Ala Glu Ala
 530 535 540
 Glu Lys Leu Leu Ala Leu Leu Lys Glu Ser Lys
 545 550 555

<210> 68
 <211> 428
 <212> PRT
 <213> S. pneumoniae

<400> 68

Asp Ile Asp Ser Leu Leu Lys Gln Leu Tyr Lys Leu Pro Leu Ser Gln
 1 5 10 15
 Arg His Val Glu Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr
 20 25 30
 Ser Arg Thr Ala Arg Gly Val Ala Val Pro His Gly Asn His Tyr His
 35 40 45
 Phe Ile Pro Tyr Glu Gln Met Ser Glu Leu Glu Lys Arg Ile Ala Arg
 50 55 60
 Ile Ile Pro Leu Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser Arg
 65 70 75 80
 Pro Glu Glu Pro Ser Pro Gln Pro Thr Pro Glu Pro Ser Pro Ser Pro
 85 90 95
 Gln Pro Ala Pro Asn Pro Gln Pro Ala Pro Ser Asn Pro Ile Asp Glu
 100 105 110
 Lys Leu Val Lys Glu Ala Val Arg Lys Val Gly Asp Gly Tyr Val Phe
 115 120 125
 Glu Glu Asn Gly Val Ser Arg Tyr Ile Pro Ala Lys Asn Leu Ser Ala
 130 135 140
 Glu Thr Ala Ala Gly Ile Asp Ser Lys Leu Ala Lys Gln Glu Ser Leu
 145 150 155 160
 Ser His Lys Leu Gly Ala Lys Lys Thr Asp Leu Pro Ser Ser Asp Arg
 165 170 175
 Glu Phe Tyr Asn Lys Ala Tyr Asp Leu Leu Ala Arg Ile His Gln Asp
 180 185 190
 Leu Leu Asp Asn Lys Gly Arg Gln Val Asp Phe Glu Ala Leu Asp Asn
 195 200 205
 Leu Leu Glu Arg Leu Lys Asp Val Ser Ser Asp Lys Val Lys Leu Val
 210 215 220
 Asp Asp Ile Leu Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg Leu
 225 230 235 240
 Gly Lys Pro Asn Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val
 245 250 255
 Ala Lys Leu Ala Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp
 260 265 270
 Pro Arg Asp Ile Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His
 275 280 285

Met Thr His Ser His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu
 290 295 300
 Arg Ala Ala Ala Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro
 305 310 315 320
 Ser Thr Asp His Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu
 325 330 335
 Ala Ile Tyr Asn Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg
 340 345 350
 Met Pro Tyr Asn Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu
 355 360 365
 Ile Ile Pro His Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe
 370 375 380
 Asp Glu Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Thr Leu Glu Asp Leu
 385 390 395 400
 Leu Ala Thr Val Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His
 405 410 415
 Ser Asp Asn Gly Phe Gly Asn Ala Ser Asp His Val
 420 425

<210> 69
 <211> 121
 <212> PRT
 <213> S. pneumoniae

<400> 69

Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu Ala
 1 5 10 15
 Thr Val Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His Ser Asp
 20 25 30
 Asn Gly Phe Gly Asn Ala Ser Asp His Val Gln Arg Asn Lys Asn Gly
 35 40 45
 Gln Ala Asp Thr Asn Gln Thr Glu Lys Pro Ser Glu Glu Lys Pro Gln
 50 55 60
 Thr Glu Lys Pro Glu Glu Thr Pro Arg Glu Glu Lys Pro Gln Ser
 65 70 75 80
 Glu Lys Pro Glu Ser Pro Lys Pro Thr Glu Glu Pro Glu Glu Glu Ser
 85 90 95
 Pro Glu Glu Ser Glu Glu Pro Gln Val Glu Thr Glu Lys Val Glu Glu
 100 105 110
 Lys Leu Arg Glu Ala Glu Asp Leu Leu
 115 120

<210> 70
 <211> 132
 <212> PRT
 <213> S. pneumoniae

<400> 70

Ala Ser Asp His Val Gln Arg Asn Lys Asn Gly Gln Ala Asp Thr Asn
 1 5 10 15
 Gln Thr Glu Lys Pro Ser Glu Glu Lys Pro Gln Thr Glu Lys Pro Glu
 20 25 30
 Glu Glu Thr Pro Arg Glu Glu Lys Pro Gln Ser Glu Lys Pro Glu Ser
 35 40 45
 Pro Lys Pro Thr Glu Glu Pro Glu Glu Glu Ser Pro Glu Glu Ser Glu
 50 55 60
 Glu Pro Gln Val Glu Thr Glu Lys Val Glu Glu Lys Leu Arg Glu Ala

65					70					75				80	
Glu	Asp	Leu	Leu	Gly	Lys	Ile	Gln	Asp	Pro	Ile	Ile	Lys	Ser	Asn	Ala
				85					90					95	
Lys	Glu	Thr	Leu	Thr	Gly	Leu	Lys	Asn	Asn	Leu	Leu	Phe	Gly	Thr	Gln
			100					105					110		
Asp	Asn	Asn	Thr	Ile	Met	Ala	Glu	Ala	Glu	Lys	Leu	Leu	Ala	Leu	Leu
		115					120						125		
Lys	Glu	Ser	Lys												
	130														

<210> 71
 <211> 226
 <212> PRT
 <213> S. pneumoniae

<400> 71

Asp	Ile	Asp	Ser	Leu	Leu	Lys	Gln	Leu	Tyr	Lys	Leu	Pro	Leu	Ser	Gln
1				5					10					15	
Arg	His	Val	Glu	Ser	Asp	Gly	Leu	Ile	Phe	Asp	Pro	Ala	Gln	Ile	Thr
			20					25					30		
Ser	Arg	Thr	Ala	Arg	Gly	Val	Ala	Val	Pro	His	Gly	Asn	His	Tyr	His
		35					40					45			
Phe	Ile	Pro	Tyr	Glu	Gln	Met	Ser	Glu	Leu	Glu	Lys	Arg	Ile	Ala	Arg
	50					55					60				
Ile	Ile	Pro	Leu	Arg	Tyr	Arg	Ser	Asn	His	Trp	Val	Pro	Asp	Ser	Arg
65					70					75					80
Pro	Glu	Glu	Pro	Ser	Pro	Gln	Pro	Thr	Pro	Glu	Pro	Ser	Pro	Ser	Pro
				85					90					95	
Gln	Pro	Ala	Pro	Asn	Pro	Gln	Pro	Ala	Pro	Ser	Asn	Pro	Ile	Asp	Glu
			100					105					110		
Lys	Leu	Val	Lys	Glu	Ala	Val	Arg	Lys	Val	Gly	Asp	Gly	Tyr	Val	Phe
		115					120					125			
Glu	Glu	Asn	Gly	Val	Ser	Arg	Tyr	Ile	Pro	Ala	Lys	Asn	Leu	Ser	Ala
	130					135						140			
Glu	Thr	Ala	Ala	Gly	Ile	Asp	Ser	Lys	Leu	Ala	Lys	Gln	Glu	Ser	Leu
145					150					155					160
Ser	His	Lys	Leu	Gly	Ala	Lys	Lys	Thr	Asp	Leu	Pro	Ser	Ser	Asp	Arg
			165						170					175	
Glu	Phe	Tyr	Asn	Lys	Ala	Tyr	Asp	Leu	Leu	Ala	Arg	Ile	His	Gln	Asp
			180					185					190		
Leu	Leu	Asp	Asn	Lys	Gly	Arg	Gln	Val	Asp	Phe	Glu	Ala	Leu	Asp	Asn
		195					200					205			
Leu	Leu	Glu	Arg	Leu	Lys	Asp	Val	Ser	Ser	Asp	Lys	Val	Lys	Leu	Val
	210					215					220				
Asp	Asp														
225															

<210> 72
 <211> 203
 <212> PRT
 <213> S. pneumoniae

<400> 72

Asp	Ile	Leu	Ala	Phe	Leu	Ala	Pro	Ile	Arg	His	Pro	Glu	Arg	Leu	Gly
1				5					10					15	
Lys	Pro	Asn	Ala	Gln	Ile	Thr	Tyr	Thr	Asp	Asp	Glu	Ile	Gln	Val	Ala
			20					25					30		

Lys Leu Ala Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro
 35 40 45
 Arg Asp Ile Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met
 50 55 60
 Thr His Ser His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg
 65 70 75 80
 Ala Ala Ala Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser
 85 90 95
 Thr Asp His Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala
 100 105 110
 Ile Tyr Asn Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met
 115 120 125
 Pro Tyr Asn Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile
 130 135 140
 Ile Pro His Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp
 145 150 155 160
 Glu Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu
 165 170 175
 Ala Thr Val Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His Ser
 180 185 190
 Asp Asn Gly Phe Gly Asn Ala Ser Asp His Val
 195 200

<210> 73
 <211> 819
 <212> PRT
 <213> S. pneumoniae

<400> 73

Cys Ser Tyr Glu Leu Gly Arg His Gln Ala Gly Gln Val Lys Lys Glu
 1 5 10 15
 Ser Asn Arg Val Ser Tyr Ile Asp Gly Asp Gln Ala Gly Gln Lys Ala
 20 25 30
 Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala
 35 40 45
 Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His
 50 55 60
 Gly Asp His Tyr His Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile
 65 70 75 80
 Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp
 85 90 95
 Ser Asp Ile Val Asn Glu Ile Lys Gly Gly Tyr Val Ile Lys Val Asp
 100 105 110
 Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Ile
 115 120 125
 Arg Thr Lys Glu Glu Ile Lys Arg Gln Lys Gln Glu His Ser His Asn
 130 135 140
 His Asn Ser Arg Ala Asp Asn Ala Val Ala Ala Ala Arg Ala Gln Gly
 145 150 155 160
 Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser Asp Ile Ile
 165 170 175
 Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asp His Tyr His
 180 185 190
 Tyr Ile Pro Lys Asn Glu Leu Ser Ala Ser Glu Leu Ala Ala Glu
 195 200 205
 Ala Tyr Trp Asn Gly Lys Gln Gly Ser Arg Pro Ser Ser Ser Ser
 210 215 220

Tyr Asn Ala Asn Pro Val Gln Pro Arg Leu Ser Glu Asn His Asn Leu
 225 230 235 240
 Thr Val Thr Pro Thr Tyr His Gln Asn Gln Gly Glu Asn Ile Ser Ser
 245 250 255
 Leu Leu Arg Glu Leu Tyr Ala Lys Pro Leu Ser Glu Arg His Val Glu
 260 265 270
 Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr Ala
 275 280 285
 Arg Gly Val Ala Val Pro His Gly Asn His Tyr His Phe Ile Pro Tyr
 290 295 300
 Glu Gln Met Ser Glu Leu Glu Lys Arg Ile Ala Arg Ile Ile Pro Leu
 305 310 315 320
 Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Gln Pro
 325 330 335
 Ser Pro Gln Ser Thr Pro Glu Pro Ser Pro Ser Leu Gln Pro Ala Pro
 340 345 350
 Asn Pro Gln Pro Ala Pro Ser Asn Pro Ile Asp Glu Lys Leu Val Lys
 355 360 365
 Glu Ala Val Arg Lys Val Gly Asp Gly Tyr Val Phe Glu Glu Asn Gly
 370 375 380
 Val Ser Arg Tyr Ile Pro Ala Lys Asp Leu Ser Ala Glu Thr Ala Ala
 385 390 395 400
 Gly Ile Asp Ser Lys Leu Ala Lys Gln Glu Ser Leu Ser His Lys Leu
 405 410 415
 Gly Ala Lys Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu Phe Tyr Asn
 420 425 430
 Lys Ala Tyr Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp Asn
 435 440 445
 Lys Gly Arg Gln Val Asp Phe Glu Val Leu Asp Asn Leu Leu Glu Arg
 450 455 460
 Leu Lys Asp Val Ser Ser Asp Lys Val Lys Leu Val Asp Asp Ile Leu
 465 470 475 480
 Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro Asn
 485 490 495
 Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
 500 505 510
 Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp Ile
 515 520 525
 Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His Ser
 530 535 540
 His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala
 545 550 555 560
 Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His
 565 570 575
 Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn
 580 585 590
 Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn
 595 600 605
 Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His
 610 615 620
 Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu
 625 630 635 640
 Tyr Glu Ala Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val
 645 650 655
 Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn Gly
 660 665 670

Phe Gly Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp Gln Asp
 675 680 685
 Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu Pro Thr
 690 695 700
 His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn Pro Ser
 705 710 715 720
 Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr Glu Glu
 725 730 735
 Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gln Val Glu Asn
 740 745 750
 Ser Val Ile Asn Ala Lys Ile Ala Asp Ala Glu Ala Leu Leu Glu Lys
 755 760 765
 Val Thr Asp Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly
 770 775 780
 Leu Lys Ser Ser Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser
 785 790 795 800
 Ala Glu Val Asp Ser Leu Leu Ala Leu Lys Glu Ser Gln Pro Ala
 805 810 815
 Pro Ile Gln

<210> 74
 <211> 568
 <212> PRT
 <213> S. pneumoniae

<400> 74

Glu Asn Ile Ser Ser Leu Leu Arg Glu Leu Tyr Ala Lys Pro Leu Ser
 1 5 10 15
 Glu Arg His Val Glu Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile
 20 25 30
 Thr Ser Arg Thr Ala Arg Gly Val Ala Val Pro His Gly Asn His Tyr
 35 40 45
 His Phe Ile Pro Tyr Glu Gln Met Ser Glu Leu Glu Lys Arg Ile Ala
 50 55 60
 Arg Ile Ile Pro Leu Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser
 65 70 75 80
 Arg Pro Glu Gln Pro Ser Pro Gln Ser Thr Pro Glu Pro Ser Pro Ser
 85 90 95
 Leu Gln Pro Ala Pro Asn Pro Gln Pro Ala Pro Ser Asn Pro Ile Asp
 100 105 110
 Glu Lys Leu Val Lys Glu Ala Val Arg Lys Val Gly Asp Gly Tyr Val
 115 120 125
 Phe Glu Glu Asn Gly Val Ser Arg Tyr Ile Pro Ala Lys Asp Leu Ser
 130 135 140
 Ala Glu Thr Ala Ala Gly Ile Asp Ser Lys Leu Ala Lys Gln Glu Ser
 145 150 155 160
 Leu Ser His Lys Leu Gly Ala Lys Lys Thr Asp Leu Pro Ser Ser Asp
 165 170 175
 Arg Glu Phe Tyr Asn Lys Ala Tyr Asp Leu Leu Ala Arg Ile His Gln
 180 185 190
 Asp Leu Leu Asp Asn Lys Gly Arg Gln Val Asp Phe Glu Val Leu Asp
 195 200 205
 Asn Leu Leu Glu Arg Leu Lys Asp Val Ser Ser Asp Lys Val Lys Leu
 210 215 220
 Val Asp Asp Ile Leu Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg
 225 230 235 240

Leu Gly Lys Pro Asn Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln
 245 250 255
 Val Ala Lys Leu Ala Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe
 260 265 270
 Asp Pro Arg Asp Ile Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro
 275 280 285
 His Met Thr His Ser His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala
 290 295 300
 Glu Arg Ala Ala Ala Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro
 305 310 315 320
 Pro Ser Thr Asp His Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala
 325 330 335
 Glu Ala Ile Tyr Asn Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp
 340 345 350
 Arg Met Pro Tyr Asn Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser
 355 360 365
 Leu Ile Ile Pro His Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp
 370 375 380
 Phe Asp Glu Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Ser Leu Glu Asp
 385 390 395 400
 Leu Leu Ala Thr Val Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro
 405 410 415
 His Ser Asp Asn Gly Phe Gly Asn Ala Ser Asp His Val Arg Lys Asn
 420 425 430
 Lys Ala Asp Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu
 435 440 445
 Val Ser Glu Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala
 450 455 460
 Gly Leu Asn Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr
 465 470 475 480
 Glu Glu Thr Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile
 485 490 495
 Pro Gln Val Glu Asn Ser Val Ile Asn Ala Lys Ile Ala Asp Ala Glu
 500 505 510
 Ala Leu Leu Glu Lys Val Thr Asp Pro Ser Ile Arg Gln Asn Ala Met
 515 520 525
 Glu Thr Leu Thr Gly Leu Lys Ser Ser Leu Leu Leu Gly Thr Lys Asp
 530 535 540
 Asn Asn Thr Ile Ser Ala Glu Val Asp Ser Leu Leu Ala Leu Leu Lys
 545 550 555 560
 Glu Ser Gln Pro Ala Pro Ile Gln
 565

<210> 75

<211> 140

<212> PRT

<213> S. pneumoniae

<400> 75

Val Arg Lys Asn Lys Ala Asp Gln Asp Ser Lys Pro Asp Glu Asp Lys
 1 5 10 15
 Glu His Asp Glu Val Ser Glu Pro Thr His Pro Glu Ser Asp Glu Lys
 20 25 30
 Glu Asn His Ala Gly Leu Asn Pro Ser Ala Asp Asn Leu Tyr Lys Pro
 35 40 45
 Ser Thr Asp Thr Glu Glu Thr Glu Glu Glu Ala Glu Asp Thr Thr Asp
 50 55 60

Glu Ala Glu Ile Pro Gln Val Glu Asn Ser Val Ile Asn Ala Lys Ile
 65 70 75 80
 Ala Asp Ala Glu Ala Leu Leu Glu Lys Val Thr Asp Pro Ser Ile Arg
 85 90 95
 Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser Ser Leu Leu Leu
 100 105 110
 Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val Asp Ser Leu Leu
 115 120 125
 Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
 130 135 140

<210> 76
 <211> 3171
 <212> DNA
 <213> *S. pneumoniae*

<400> 76

gacttgacag aagagcaa ataggctgcg caaaaacatt tagaggaagt taaaactagt 60
 cataatggat tagattcttt gtcattctcat gaacaggatt atccaggtaa tgccaaagaa 120
 atgaaagatt tagataaaaa aatcgaagaa aaaattgctg gcattatgaa acaatatggt 180
 gtcaaactgt aaagtattgt cgtgaataaa gaaaaaaatg cgattattta tccgcatgga 240
 gatcaccatc atgcagatcc gattgatgaa cataaacagg ttggaattgg tcattctcac 300
 agtaactatg aactgtttta acccgaagaa ggagttgcta aaaaagaagg gaataaagtt 360
 tatactggag aagaattaac gaatgttggt aatttggtta aaaatagtag gtttaataat 420
 caaaacttta ctctagccaa tggcctcaaaa cgcgtttctt ttagttttcc gcctgaattg 480
 gagaaaaaat taggtatcaa tatgctagta aaattaataa caccagatgg aaaagtattg 540
 gagaaagtat ctggtaaagt atttggagaa ggagtaggga atattgcaa ctttgaatta 600
 gatcaacctt atttaccagg acaaacattt aagtatacta tcgcttcaa agattatcca 660
 gaagtaagtt atgatggtac atttacagtt ccaacctctt tagcttaca aatggccagt 720
 caaacgattt tctatccttt ccatgcaggg gatacttatt taagagtga ccctcaattt 780
 gcagtgccta aaggaactga tgcttttagtc agagtgtttg atgaatttca tggaaatgct 840
 tatttagaaa ataactataa agttggtgaa atcaaattac cgattccgaa attaaaccaa 900
 ggaacaacca gaacggccgg aaataaaaatt cctgtaacct tcatggcaa tgcttatttg 960
 gacaatcaat cgacttatat tgtggaagta cctatcttgg aaaaagaaaa tcaaactgat 1020
 aaaccaagta ttctaccaca atttaaaagg aataaagcag aagaaaactc aaaacttgat 1080
 gaaaaggtag aagaaccaa gactagttag aaggtagaaa aagaaaaact ttctgaaact 1140
 gggaatagta ctagtaattc aacgttagaa gaagttccta cagtggatcc tgtacaagaa 1200
 aaagttagcaa aatttgctga aagttatggg atgaagctag aaaatgtctt gtttaatatg 1260
 gacggaacaa ttgaattata ttaccatca ggagaagtca ttaaaaagaa tatggcagat 1320
 ttacaggag aagcacctca aggaaatggt gaaaataaac catctgaaa tggaaaagta 1380
 tctactggaa cagttgagaa ccaaccaaca gaaaataaac cagcagattc ttaccagag 1440
 gcaccaaacg aaaaacctgt aaaaccagaa aactcaacgg ataattggaat gttgaatcca 1500
 gaaggggaatg tggggagtga ccctatgtta gatccagcat tagaggaagc tccagcagta 1560
 gatcctgtac aagaaaaatt agaaaaattt acagctagtt acggattagg cttagatagt 1620
 gttatattca atatggatgg aacgattgaa ttaagattgc caagtggaga agtgataaaa 1680
 aagaatttat ctgatttcat agcgaagctt cgttatcggt caaaccattg ggtaccagat 1740
 tcaagaccag aagaaccaag tccacaaccg actccagaac ctagtccaag tccgcaacct 1800
 gcaccaaact ctcaaccagc tccaagcaat ccaattgatg agaaattggt caaagaagct 1860
 gttcgaaaag taggcgatgg ttatgtcttt gaggagaatg gagtttctcg ttatatccca 1920
 gccaaagaatc ttctagcaga aacagcagca ggcattgata gcaaactggc caagcaggaa 1980
 agtttatctc ataagctagg agctaagaaa actgacctcc catctagtga tcgagaattt 2040
 tacaataagg cttatgactt actagcaaga attcaccaag atttacttga taataaaggt 2100
 cgacaagttg attttgaggc tttggataac ctggttggaac gactcaagga tgtctcaagt 2160
 gataaagtca agttagtggg tgatattctt gccttcttag ctccgattcg tcattccagaa 2220
 cgtttaggaa aaccaaatgc gcaaattacc tacactgatg atgagattca agtagccaag 2280
 ttggcaggca agtacacaac agaagacggg tatatctttg atcctcgtga tataaccagt 2340
 gatgaggggg atgcctatgt aactccacat atgaccata gccactggat taaaaaagat 2400

```

agtttgtctg aagctgagag agcggcagcc caggcttatg ctaaagagaa aggtttgacc 2460
cctccttcga cagaccatca ggattcagga aatactgagg caaaaggagc agaagctatc 2520
tacaaccgcg tgaaagcagc taagaaggtg ccacttgatc gtatgcctta caatcttcaa 2580
tatactgtag aagtcaaaaa cggtagttaa atcatacctc attatgacca ttaccataac 2640
atcaaatttg agtggtttga cgaaggcctt tatgaggcac ctaaggggta tactcttgag 2700
gatcttttgg cgactgtcaa gtactatgtc gaacatccaa acgaacgtcc gcattcagat 2760
aatgggtttg gtaacgctag cgaccatgtt caaagaaaca aaaatgggtca agctgatacc 2820
aatcaaacgg aaaaaccaag cgaggagaaa cctcagacag aaaaacctga ggaagaaacc 2880
cctcgagaag agaaaccaca aagcgagaaa ccagagtctc caaaaccaac agaggaacca 2940
gaagaagaat caccagagga atcagaagaa cctcaggtcg agactgaaaa ggttgaagaa 3000
aaactgagag aggctgaaga tttacttgga aaaatccagg atccaattat caagtccaat 3060
gccaaagaga ctctcacagg attaaaaaat aattttactat ttggcaccca ggacaacaat 3120
actattatgg cagaagctga aaaactattg gctttattaa aggagagtaa g 3171

```


<210> 77

<211> 473

<212> PRT

<213> S. pneumoniae

<400> 77



```

Glu Ala Tyr Trp Asn Gly Lys Gln Gly Ser Arg Pro Ser Ser Ser Ser
 1          5          10          15
Ser Tyr Asn Ala Asn Pro Val Gln Pro Arg Leu Ser Glu Asn His Asn
          20          25          30
Leu Thr Val Thr Pro Thr Tyr His Gln Asn Gln Gly Glu Asn Ile Ser
          35          40          45
Ser Leu Leu Arg Glu Leu Tyr Ala Lys Pro Leu Ser Glu Arg His Val
          50          55          60
Glu Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr
65          70          75          80
Ala Arg Gly Val Ala Val Pro His Gly Asn His Tyr His Phe Ile Pro
          85          90          95
Tyr Glu Gln Met Ser Glu Leu Glu Lys Arg Ile Ala Arg Ile Ile Pro
          100          105          110
Leu Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Gln
          115          120          125
Pro Ser Pro Gln Ser Thr Pro Glu Pro Ser Pro Ser Leu Gln Pro Ala
          130          135          140
Pro Asn Pro Gln Pro Ala Pro Ser Asn Pro Ile Asp Glu Lys Leu Val
145          150          155          160
Lys Glu Ala Val Arg Lys Val Gly Asp Gly Tyr Val Phe Glu Glu Asn
          165          170          175
Gly Val Ser Arg Tyr Ile Pro Ala Lys Asp Leu Ser Ala Glu Thr Ala
          180          185          190
Ala Gly Ile Asp Ser Lys Leu Ala Lys Gln Glu Ser Leu Ser His Lys
          195          200          205
Leu Gly Ala Lys Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu Phe Tyr
          210          215          220
Asn Lys Ala Tyr Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp
225          230          235          240
Asn Lys Gly Arg Gln Val Asp Phe Glu Val Leu Asp Asn Leu Leu Glu
          245          250          255
Arg Leu Lys Asp Val Ser Ser Asp Lys Val Lys Leu Val Asp Asp Ile
          260          265          270
Leu Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro
          275          280          285

```

Asn Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu
 290 295 300
 Ala Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp
 305 310 315 320
 Ile Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His
 325 330 335
 Ser His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala
 340 345 350
 Ala Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp
 355 360 365
 His Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr
 370 375 380
 Asn Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr
 385 390 395 400
 Asn Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro
 405 410 415
 His Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly
 420 425 430
 Leu Tyr Glu Ala Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr
 435 440 445
 Val Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn
 450 455 460
 Gly Phe Gly Asn Ala Ser Asp His Val
 465 470

<210> 78
 <211> 780
 <212> PRT
 <213> S. pneumoniae

<400> 78
 Cys Ala Tyr Ala Leu Asn Gln His Arg Ser Gln Glu Asn Lys Asp Asn
 1 5 10 15
 Asn Arg Val Ser Tyr Val Asp Gly Ser Gln Ser Ser Gln Lys Ser Glu
 20 25 30
 Asn Leu Thr Pro Asp Gln Val Ser Gln Lys Glu Gly Ile Gln Ala Glu
 35 40 45
 Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly
 50 55 60
 Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Leu Phe
 65 70 75 80
 Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp Ala
 85 90 95
 Asp Ile Val Asn Glu Val Lys Gly Gly Tyr Ile Ile Lys Val Asp Gly
 100 105 110
 Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg
 115 120 125
 Thr Lys Asp Glu Ile Asn Arg Gln Lys Gln Glu His Val Lys Asp Asn
 130 135 140
 Glu Lys Val Asn Ser Asn Val Ala Val Ala Arg Ser Gln Gly Arg Tyr
 145 150 155 160
 Thr Thr Asn Asp Gly Tyr Val Phe Asn Pro Ala Asp Ile Ile Glu Asp
 165 170 175
 Thr Gly Asn Ala Tyr Ile Val Pro His Gly Gly His Tyr His Tyr Ile
 180 185 190
 Pro Lys Ser Asp Leu Ser Ala Ser Glu Leu Ala Ala Ala Lys Ala His
 195 200 205

Leu Ala Gly Lys Asn Met Gln Pro Ser Gln Leu Ser Tyr Ser Ser Thr
 210 215 220
 Ala Ser Asp Asn Asn Thr Gln Ser Val Ala Lys Gly Ser Thr Ser Lys
 225 230 235 240
 Pro Ala Asn Lys Ser Glu Asn Leu Gln Ser Leu Leu Lys Glu Leu Tyr
 245 250 255
 Asp Ser Pro Ser Ala Gln Arg Tyr Ser Glu Ser Asp Gly Leu Val Phe
 260 265 270
 Asp Pro Ala Lys Ile Ile Ser Arg Thr Pro Asn Gly Val Ala Ile Pro
 275 280 285
 His Gly Asp His Tyr His Phe Ile Pro Tyr Ser Lys Leu Ser Ala Leu
 290 295 300
 Glu Glu Lys Ile Ala Arg Met Val Pro Ile Ser Gly Thr Gly Ser Thr
 305 310 315 320
 Val Ser Thr Asn Ala Lys Pro Asn Glu Val Val Ser Ser Leu Gly Ser
 325 330 335
 Leu Ser Ser Asn Pro Ser Ser Leu Thr Thr Ser Lys Glu Leu Ser Ser
 340 345 350
 Ala Ser Asp Gly Tyr Ile Phe Asn Pro Lys Asp Ile Val Glu Glu Thr
 355 360 365
 Ala Thr Ala Tyr Ile Val Arg His Gly Asp His Phe His Tyr Ile Pro
 370 375 380
 Lys Ser Asn Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala
 385 390 395 400
 Thr Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys
 405 410 415
 His Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu
 420 425 430
 Asp Glu Ser Gly Phe Val Met Ser His Gly Asp His Asn His Tyr Phe
 435 440 445
 Phe Lys Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His
 450 455 460
 Leu Glu Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser
 465 470 475 480
 His Glu Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp
 485 490 495
 Lys Lys Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val
 500 505 510
 Lys Arg Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr
 515 520 525
 Pro His Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro
 530 535 540
 Val Gly Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu
 545 550 555 560
 Glu Gly Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu
 565 570 575
 Leu Thr Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln
 580 585 590
 Asn Phe Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro
 595 600 605
 Pro Glu Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile
 610 615 620
 Thr Pro Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly
 625 630 635 640
 Glu Gly Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu
 645 650 655

Pro Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu
660 665 670
Val Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys
675 680 685
Met Ala Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr
690 695 700
Leu Arg Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu
705 710 715 720
Val Arg Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn
725 730 735
Tyr Lys Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly
740 745 750
Thr Thr Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn
755 760 765
Ala Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu
770 775 780

<210> 79
<211> 690
<212> PRT
<213> S. pneumoniae

<400> 79

Cys Ala Tyr Glu Leu Gly Leu His Gln Ala Gln Thr Val Lys Glu Asn
1 5 10 15
Asn Arg Val Ser Tyr Ile Asp Gly Lys Gln Ala Thr Gln Lys Thr Glu
20 25 30
Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala Glu
35 40 45
Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly
50 55 60
Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile Ile
65 70 75 80
Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp Ser
85 90 95
Asp Ile Val Asn Glu Ile Lys Gly Gly Tyr Val Ile Lys Val Asn Gly
100 105 110
Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg
115 120 125
Thr Lys Glu Glu Ile Asn Arg Gln Lys Gln Glu His Ser Gln His Arg
130 135 140
Glu Gly Gly Thr Ser Ala Asn Asp Gly Ala Val Ala Phe Ala Arg Ser
145 150 155 160
Gln Gly Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser Asp
165 170 175
Ile Ile Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asp His
180 185 190
Tyr His Tyr Ile Pro Lys Asn Glu Leu Ser Ala Ser Glu Leu Ala Ala
195 200 205
Ala Glu Ala Phe Leu Ser Gly Arg Glu Asn Leu Ser Asn Leu Arg Thr
210 215 220
Tyr Arg Arg Gln Asn Ser Asp Asn Thr Pro Arg Thr Asn Trp Val Pro
225 230 235 240
Ser Val Ser Asn Pro Gly Thr Thr Asn Thr Asn Thr Ser Asn Asn Ser
245 250 255
Asn Thr Asn Ser Gln Ala Ser Gln Ser Asn Asp Ile Asp Ser Leu Leu
260 265 270

Lys Gln Leu Tyr Lys Leu Pro Leu Ser Gln Arg His Val Glu Ser Asp
 275 280 285
 Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr Ala Arg Gly
 290 295 300
 Val Ala Val Pro His Gly Asn His Tyr His Phe Ile Pro Tyr Glu Gln
 305 310 315 320
 Met Ser Glu Leu Glu Lys Arg Ile Ala Arg Ile Ile Pro Leu Arg Tyr
 325 330 335
 Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Glu Pro Ser Pro
 340 345 350
 Gln Pro Thr Pro Glu Pro Ser Pro Ser Pro Gln Pro Ala Pro Asn Pro
 355 360 365
 Gln Pro Ala Pro Ser Asn Pro Ile Asp Glu Lys Leu Val Lys Glu Ala
 370 375 380
 Val Arg Lys Val Gly Asp Gly Tyr Val Phe Glu Glu Asn Gly Val Ser
 385 390 395 400
 Arg Tyr Ile Pro Ala Lys Asn Leu Ser Ala Glu Thr Ala Ala Gly Ile
 405 410 415
 Asp Ser Lys Leu Ala Lys Gln Glu Ser Leu Ser His Lys Leu Gly Ala
 420 425 430
 Lys Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu Phe Tyr Asn Lys Ala
 435 440 445
 Tyr Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp Asn Lys Gly
 450 455 460
 Arg Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu Arg Leu Lys
 465 470 475 480
 Asp Val Ser Ser Asp Lys Val Lys Leu Val Asp Asp Ile Leu Ala Phe
 485 490 495
 Leu Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro Asn Ala Gln
 500 505 510
 Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala Gly Lys
 515 520 525
 Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp Ile Thr Ser
 530 535 540
 Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His Ser His Trp
 545 550 555 560
 Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala
 565 570 575
 Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp
 580 585 590
 Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val
 595 600 605
 Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln
 610 615 620
 Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His Tyr Asp
 625 630 635 640
 His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu
 645 650 655
 Ala Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr
 660 665 670
 Tyr Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn Gly Phe Gly
 675 680 685
 Asn Ala
 690

<210> 80
 <211> 2469
 <212> DNA
 <213> *S. pneumoniae*

<400> 80

gtgaagaaaa catatgggta tatcgggtca gttgctgcca ttttactagc tactcatatt 60
 ggaagttacc aacttggtaa gcatcatatg ggtctagcaa caaaggacaa tcagattgcc 120
 tatattgatg acagcaaagg taaggcaaaa gccctataaa caaacaaaac gatggatcaa 180
 atcagtgtcg aagaaggcat ctctgctgaa cagatcgtag tcaaaattac tgaccaaggc 240
 tatgtgacct cacacgggtga ccattatcat ttttacaatg ggaaagttcc ttatgatgcg 300
 attattagtg aagagttggt gatgacggat cctaattacc gtttttaaca atcagacgtt 360
 atcaatgaaa tcttagacgg ttacgttatt aaagtcaatg gcaactatta tgtttacctc 420
 aagccaggta gtaagcgcaa aaacattcga accaaacaac aaattgctga gcaagtagcc 480
 aaaggaaacta agaagctaa agaaaaaggt ttagctcaag tggcccatct cagtaaagaa 540
 gaagttgcgg cagtcaatga agcaaaaaa caaggacgct atactacaga cgatggctat 600
 atttttagtc cgacagatat cattgatgat ttaggagatg cttatttagt acctcatggt 660
 aatcactatc attatattcc taaaaaggat ttgtctccaa gtgagctagc tgctgcacaa 720
 gcctactgga gtcaaaaaa aggtcgaggt gctagaccgt ctgattaccg cccgacacca 780
 gccccagggtc gtaggaaagc cccaattcct gatgtgacgc ctaaccctgg acaaggtcat 840
 cagccagata acggtgggcta tcatccagcg cctcctaggc caaatgatgc gtcacaaaaac 900
 aaacacccaaa gagatgagtt taaaggaaaa acctttaagg aactttttaga tcaactacac 960
 cgtcttgatt tgaaataccg tcatgtggaa gaagatgggt tgatttttga accgactcaa 1020
 gtgatcaaat caaacgcttt tgggtatgtg gtgcctcatg gagatcatta tcatattatc 1080
 ccaagaagtc agttatcacc tcttgaaatg gaattagcag atcgatactt agctggccaa 1140
 actgaggaca atgactcagg ttcagagcac tcaaaaccat cagataaaga agtgacacat 1200
 acctttcttg gtcacgcgat caaagcttac ggaaaaggct tagatggtaa accatatgat 1260
 acgagtgatg cttatgtttt tagtaaagaa tccattcatt cagtggataa atcaggagtt 1320
 acagctaaac acggagatca tttccactat ataggatttg gagaacttga acaatatgag 1380
 ttggatgagg tcgctaactg ggtgaaagca aaagggtcaag ctgatgagct tgctgctgct 1440
 ttggatcagg aacaaggcaa agaaaaacca ctctttgaca ctaaaaaagt gagtcgcaaa 1500
 gtaacaaaag atggtaaagt gggctatatg atgccaaaag atggtaagga ctatttctat 1560
 gctcgtgatc aacttgattt gactcagatt gcctttgccg aacaagaact aatgcttaaa 1620
 gataagaagc attaccgtta tgacattggt gacacaggta ttgagccacg acttgctgta 1680
 gatgtgtcaa gtctgccgat gcatgctggt aatgctactt acgatactgg aagttcgttt 1740
 gttatccca atattgatca tatccatgtc gttccgtatt catggttgac gcgcatcag 1800
 attgcaacag tcaagtatgt gatgcaacac cccgaagttc gtccggatgt atggtctaag 1860
 ccagggcatg aagagtcagg ttcggtcatt ccaaatgtta cgctcttga taaacgtgct 1920
 ggtatgccaa actggcgaat tatccattct gctgaagaag ttcaaaaagc cctagcagaa 1980
 ggtcgttttg caacaccaga cggctatat ttcgatccac gagatgtttt ggccaaaagaa 2040
 acttttgtat ggaaagatgg ctcccttagc atcccaagag cagatggcag ttcattgaga 2100
 accattaata aatctgatct atcccaagct gagtggcaac aagctcaaga gttattggca 2160
 aagaaaaata ctggtgatgc tactgatacg gataaaacca aagaaaagca acaggcagat 2220
 aagagcaatg aaaaccaaca gccaaagtga gccagtaaag aagaaaaaga atcagatgac 2280
 tttatagaca gtttaccaga ctatggtcta gatagagcaa ccctagaaga tcatatcaat 2340
 caattagcac aaaaagctaa tatcgatcct aagtatctca ttttccaacc agaaggtgtc 2400
 caattttata ataaaaatgg tgaattggta acttatgata tcaagacact tcaacaaata 2460
 aacccttaa 2469

<210> 81
 <211> 823
 <212> PRT
 <213> *S. pneumoniae*

<400> 81

Val Lys Lys Thr Tyr Gly Tyr Ile Gly Ser Val Ala Ala Ile Leu Leu
 1 5 10 15

Ala Thr His Ile Gly Ser Tyr Gln Leu Gly Lys His His Met Gly Leu
20 25 30
Ala Thr Lys Asp Asn Gln Ile Ala Tyr Ile Asp Asp Ser Lys Gly Lys
35 40 45
Ala Lys Ala Pro Lys Thr Asn Lys Thr Met Asp Gln Ile Ser Ala Glu
50 55 60
Glu Gly Ile Ser Ala Glu Gln Ile Val Val Lys Ile Thr Asp Gln Gly
65 70 75 80
Tyr Val Thr Ser His Gly Asp His Tyr His Phe Tyr Asn Gly Lys Val
85 90 95
Pro Tyr Asp Ala Ile Ile Ser Glu Glu Leu Leu Met Thr Asp Pro Asn
100 105 110
Tyr Arg Phe Lys Gln Ser Asp Val Ile Asn Glu Ile Leu Asp Gly Tyr
115 120 125
Val Ile Lys Val Asn Gly Asn Tyr Tyr Val Tyr Leu Lys Pro Gly Ser
130 135 140
Lys Arg Lys Asn Ile Arg Thr Lys Gln Gln Ile Ala Glu Gln Val Ala
145 150 155 160
Lys Gly Thr Lys Glu Ala Lys Glu Lys Gly Leu Ala Gln Val Ala His
165 170 175
Leu Ser Lys Glu Glu Val Ala Ala Val Asn Glu Ala Lys Arg Gln Gly
180 185 190
Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Ser Pro Thr Asp Ile Ile
195 200 205
Asp Asp Leu Gly Asp Ala Tyr Leu Val Pro His Gly Asn His Tyr His
210 215 220
Tyr Ile Pro Lys Lys Asp Leu Ser Pro Ser Glu Leu Ala Ala Ala Gln
225 230 235 240
Ala Tyr Trp Ser Gln Lys Gln Gly Arg Gly Ala Arg Pro Ser Asp Tyr
245 250 255
Arg Pro Thr Pro Ala Pro Gly Arg Arg Lys Ala Pro Ile Pro Asp Val
260 265 270
Thr Pro Asn Pro Gly Gln Gly His Gln Pro Asp Asn Gly Gly Tyr His
275 280 285
Pro Ala Pro Pro Arg Pro Asn Asp Ala Ser Gln Asn Lys His Gln Arg
290 295 300
Asp Glu Phe Lys Gly Lys Thr Phe Lys Glu Leu Leu Asp Gln Leu His
305 310 315 320
Arg Leu Asp Leu Lys Tyr Arg His Val Glu Glu Asp Gly Leu Ile Phe
325 330 335
Glu Pro Thr Gln Val Ile Lys Ser Asn Ala Phe Gly Tyr Val Val Pro
340 345 350
His Gly Asp His Tyr His Ile Ile Pro Arg Ser Gln Leu Ser Pro Leu
355 360 365
Glu Met Glu Leu Ala Asp Arg Tyr Leu Ala Gly Gln Thr Glu Asp Asn
370 375 380
Asp Ser Gly Ser Glu His Ser Lys Pro Ser Asp Lys Glu Val Thr His
385 390 395 400
Thr Phe Leu Gly His Arg Ile Lys Ala Tyr Gly Lys Gly Leu Asp Gly
405 410 415
Lys Pro Tyr Asp Thr Ser Asp Ala Tyr Val Phe Ser Lys Glu Ser Ile
420 425 430
His Ser Val Asp Lys Ser Gly Val Thr Ala Lys His Gly Asp His Phe
435 440 445
His Tyr Ile Gly Phe Gly Glu Leu Glu Gln Tyr Glu Leu Asp Glu Val
450 455 460

Ala Asn Trp Val Lys Ala Lys Gly Gln Ala Asp Glu Leu Ala Ala Ala
 465 470 475 480
 Leu Asp Gln Glu Gln Gly Lys Glu Lys Pro Leu Phe Asp Thr Lys Lys
 485 490 495
 Val Ser Arg Lys Val Thr Lys Asp Gly Lys Val Gly Tyr Met Met Pro
 500 505 510
 Lys Asp Gly Lys Asp Tyr Phe Tyr Ala Arg Asp Gln Leu Asp Leu Thr
 515 520 525
 Gln Ile Ala Phe Ala Glu Gln Glu Leu Met Leu Lys Asp Lys Lys His
 530 535 540
 Tyr Arg Tyr Asp Ile Val Asp Thr Gly Ile Glu Pro Arg Leu Ala Val
 545 550 555 560
 Asp Val Ser Ser Leu Pro Met His Ala Gly Asn Ala Thr Tyr Asp Thr
 565 570 575
 Gly Ser Ser Phe Val Ile Pro His Ile Asp His Ile His Val Val Pro
 580 585 590
 Tyr Ser Trp Leu Thr Arg Asp Gln Ile Ala Thr Val Lys Tyr Val Met
 595 600 605
 Gln His Pro Glu Val Arg Pro Asp Val Trp Ser Lys Pro Gly His Glu
 610 615 620
 Glu Ser Gly Ser Val Ile Pro Asn Val Thr Pro Leu Asp Lys Arg Ala
 625 630 635 640
 Gly Met Pro Asn Trp Gln Ile Ile His Ser Ala Glu Glu Val Gln Lys
 645 650 655
 Ala Leu Ala Glu Gly Arg Phe Ala Thr Pro Asp Gly Tyr Ile Phe Asp
 660 665 670
 Pro Arg Asp Val Leu Ala Lys Glu Thr Phe Val Trp Lys Asp Gly Ser
 675 680 685
 Phe Ser Ile Pro Arg Ala Asp Gly Ser Ser Leu Arg Thr Ile Asn Lys
 690 695 700
 Ser Asp Leu Ser Gln Ala Glu Trp Gln Gln Ala Gln Glu Leu Leu Ala
 705 710 715 720
 Lys Lys Asn Thr Gly Asp Ala Thr Asp Thr Asp Lys Pro Lys Glu Lys
 725 730 735
 Gln Gln Ala Asp Lys Ser Asn Glu Asn Gln Gln Pro Ser Glu Ala Ser
 740 745 750
 Lys Glu Glu Lys Glu Ser Asp Asp Phe Ile Asp Ser Leu Pro Asp Tyr
 755 760 765
 Gly Leu Asp Arg Ala Thr Leu Glu Asp His Ile Asn Gln Leu Ala Gln
 770 775 780
 Lys Ala Asn Ile Asp Pro Lys Tyr Leu Ile Phe Gln Pro Glu Gly Val
 785 790 795 800
 Gln Phe Tyr Asn Lys Asn Gly Glu Leu Val Thr Tyr Asp Ile Lys Thr
 805 810 815
 Leu Gln Gln Ile Asn Pro Pro
 820

<210> 82
 <211> 2472
 <212> DNA
 <213> S. pneumoniae

<400> 82

gtgaagaaaa	catatgggta	tatcggtca	gttgctgcca	ttttactagc	tactcatatt	60
ggaagttacc	aacttggtaa	gcatcatatg	ggcttagcaa	caaaggacaa	tcagattgcc	120
tatattgatg	atagcaaagg	taaggcaaaa	gccctaaaa	caaacaaaac	gatggatcaa	180
atcagtgcgtg	aagaaggcat	ctctgctgaa	cagatcgtag	tcaaaattac	tgaccaaggt	240

tatgtgacct cacacggtga ccattatcat ttttacaatg ggaaagtcc ttatgatgcg 300
 attattagt aagagttgtt gatgacggat cctaattacc attttaaaca atcagacggt 360
 atcaatgaaa tcttagacgg ttacgttatt aaagtcaatg gcaactatta tgtttacctc 420
 aagccaggta gtaagcgcaa aaacattcga accaaacaac aaattgctga gcaagtagcc 480
 aaaggaacta aagaagctaa agaaaaaggt ttagctcaag tggcccatct cagtaaagaa 540
 gaagttgcgg cagtcaatga agcaaaaaga caaggacgct atactacaga cgatggctat 600
 attttttagtc cgacagatat cattgatgat ttaggagacg cttatttagt acctcatggt 660
 aatcactatc atttatattcc taaaaaagat ttgtctccaa gtgagctagc tgctgcacaa 720
 gcttactgga gtcaaaaaca aggtcgaggt gctagaccgt ctgattaccg cccgacacca 780
 gccccaggtc gtaggaaagc tccaattcct gatgtgacgc ctaaccctgg acaagggtcat 840
 cagccagata acggtggcta tcatccagcg cctcctaggc caaatgatgc gtcacaaaac 900
 aaacacccaaa gagatgagtt taaaggaaaa acctttaagg aactttttaga tcaactacac 960
 cgtcttgatt tgaaataccg tcatgtggaa gaagatgggt tgatttttga accgactcaa 1020
 gtgatcaaat caaacgcttt tgggtatgtg gtgcctcatg gagatcatta tcatattatc 1080
 ccaagaagtc agttatcacc tcttgaaatg gaattagcag atcgatactt agccgggtcaa 1140
 actgaggaca atgattcagg ttcagatcac tcaaaacccat cagataaaga agtgacacat 1200
 acctttcttg gtcatcgcat caaagcttac ggaaaaggct tagatggtaa accatatgat 1260
 acgagtgatg cttatgtttt tagtaaaaga tccattcatt cagtggataa atcaggagtt 1320
 acagctaaac acggagatca tttccactat ataggatttg gagaacttga acaattagag 1380
 ttggatgagg tgcgtaactg ggtgaaagca aaagggtcaag ctgatgagct tgcgtgctgct 1440
 ttggatcagg aacaaggcaa agaaaaacca ctctttgaca ctaaaaaagt gagtgcgcaa 1500
 gtaacaaaag atggtaaaag gggctatatt atgccaaaag atggcaagga ctatttctat 1560
 gctcgtgatc aacttgattt gactcagatt gcctttgccg aacaagaact aatgcttaaa 1620
 gataagaacc attaccgtta tgacattggt gacacaggta ttgagccacg acttgctgta 1680
 gatgtgtcaa gtctgccgat gcatgctggt aatgctactt acgatactgg aagttcgttt 1740
 gttatccctc atattgatca tatccatgtc gttccgtatt catggttgac gcgcgatcag 1800
 attgcaacaa tcaagtatgt gatgcaacac cccgaagttc gtccagatgt atggtctaag 1860
 ccagggcatg aagagtcagg ttcggtcatt ccaaagtta cgcctcttga taaacgtgct 1920
 ggtatgccaa attggcaaatt catccattct gctgaagaag ttcaaaaagc cctagcagaa 1980
 ggtcgttttg caacaccaga cggctatatt ttcgatccac gagatgtttt ggccaaagaa 2040
 acttttgtat ggaaagatgg ctcccttagc atcccaagag cagatggcag ttcattgaga 2100
 accattaata aatctgatct atcccaagct gagtggcaac aagctcaaga gttattggca 2160
 aagaaaaacg ctggtgatgc tactgatagc gataaaccca aagaaaagca acaggcagat 2220
 aagagcaatg aaaaccaaca gccaaagtga gccagtaaag aagaagaaaa agaatacagat 2280
 gactttatag acagtttacc agactatggt ctagatagag caaccctaga agatcatatc 2340
 aatcaattag cacaaaaagc taatatcgat cctaagtatc tcattttcca accagaaggt 2400
 gtccaatttt ataataaaaa tgggtgaatta gtaacttatg atatcaagac gtttcaacaa 2460
 ataaaccctt aa 2472

<210> 83

<211> 824

<212> PRT

<213> S. pneumoniae

<400> 83

Val Lys Lys Thr Tyr Gly Tyr Ile Gly Ser Val Ala Ala Ile Leu Leu
 1 5 10 15
 Ala Thr His Ile Gly Ser Tyr Gln Leu Gly Lys His His Met Gly Leu
 20 25 30
 Ala Thr Lys Asp Asn Gln Ile Ala Tyr Ile Asp Asp Ser Lys Gly Lys
 35 40 45
 Ala Lys Ala Pro Lys Thr Asn Lys Thr Met Asp Gln Ile Ser Ala Glu
 50 55 60
 Glu Gly Ile Ser Ala Glu Gln Ile Val Val Lys Ile Thr Asp Gln Gly
 65 70 75 80
 Tyr Val Thr Ser His Gly Asp His Tyr His Phe Tyr Asn Gly Lys Val
 85 90 95

Pro Tyr Asp Ala Ile Ile Ser Glu Glu Leu Leu Met Thr Asp Pro Asn
 100 105 110
 Tyr His Phe Lys Gln Ser Asp Val Ile Asn Glu Ile Leu Asp Gly Tyr
 115 120 125
 Val Ile Lys Val Asn Gly Asn Tyr Tyr Val Tyr Leu Lys Pro Gly Ser
 130 135 140
 Lys Arg Lys Asn Ile Arg Thr Lys Gln Gln Ile Ala Glu Gln Val Ala
 145 150 155 160
 Lys Gly Thr Lys Glu Ala Lys Glu Lys Gly Leu Ala Gln Val Ala His
 165 170 175
 Leu Ser Lys Glu Glu Val Ala Ala Val Asn Glu Ala Lys Arg Gln Gly
 180 185 190
 Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Ser Pro Thr Asp Ile Ile
 195 200 205
 Asp Asp Leu Gly Asp Ala Tyr Leu Val Pro His Gly Asn His Tyr His
 210 215 220
 Tyr Ile Pro Lys Lys Asp Leu Ser Pro Ser Glu Leu Ala Ala Ala Gln
 225 230 235 240
 Ala Tyr Trp Ser Gln Lys Gln Gly Arg Gly Ala Arg Pro Ser Asp Tyr
 245 250 255
 Arg Pro Thr Pro Ala Pro Gly Arg Arg Lys Ala Pro Ile Pro Asp Val
 260 265 270
 Thr Pro Asn Pro Gly Gln Gly His Gln Pro Asp Asn Gly Gly Tyr His
 275 280 285
 Pro Ala Pro Pro Arg Pro Asn Asp Ala Ser Gln Asn Lys His Gln Arg
 290 295 300
 Asp Glu Phe Lys Gly Lys Thr Phe Lys Glu Leu Leu Asp Gln Leu His
 305 310 315 320
 Arg Leu Asp Leu Lys Tyr Arg His Val Glu Glu Asp Gly Leu Ile Phe
 325 330 335
 Glu Pro Thr Gln Val Ile Lys Ser Asn Ala Phe Gly Tyr Val Val Pro
 340 345 350
 His Gly Asp His Tyr His Ile Ile Pro Arg Ser Gln Leu Ser Pro Leu
 355 360 365
 Glu Met Glu Leu Ala Asp Arg Tyr Leu Ala Gly Gln Thr Glu Asp Asn
 370 375 380
 Asp Ser Gly Ser Asp His Ser Lys Pro Ser Asp Lys Glu Val Thr His
 385 390 395 400
 Thr Phe Leu Gly His Arg Ile Lys Ala Tyr Gly Lys Gly Leu Asp Gly
 405 410 415
 Lys Pro Tyr Asp Thr Ser Asp Ala Tyr Val Phe Ser Lys Glu Ser Ile
 420 425 430
 His Ser Val Asp Lys Ser Gly Val Thr Ala Lys His Gly Asp His Phe
 435 440 445
 His Tyr Ile Gly Phe Gly Glu Leu Glu Gln Tyr Glu Leu Asp Glu Val
 450 455 460
 Ala Asn Trp Val Lys Ala Lys Gly Gln Ala Asp Glu Leu Ala Ala Ala
 465 470 475 480
 Leu Asp Gln Glu Gln Gly Lys Glu Lys Pro Leu Phe Asp Thr Lys Lys
 485 490 495
 Val Ser Arg Lys Val Thr Lys Asp Gly Lys Val Gly Tyr Ile Met Pro
 500 505 510
 Lys Asp Gly Lys Asp Tyr Phe Tyr Ala Arg Asp Gln Leu Asp Leu Thr
 515 520 525
 Gln Ile Ala Phe Ala Glu Gln Glu Leu Met Leu Lys Asp Lys Asn His
 530 535 540

Tyr Arg Tyr Asp Ile Val Asp Thr Gly Ile Glu Pro Arg Leu Ala Val
 545 550 555 560
 Asp Val Ser Ser Leu Pro Met His Ala Gly Asn Ala Thr Tyr Asp Thr
 565 570 575
 Gly Ser Ser Phe Val Ile Pro His Ile Asp His Ile His Val Val Pro
 580 585 590
 Tyr Ser Trp Leu Thr Arg Asp Gln Ile Ala Thr Ile Lys Tyr Val Met
 595 600 605
 Gln His Pro Glu Val Arg Pro Asp Val Trp Ser Lys Pro Gly His Glu
 610 615 620
 Glu Ser Gly Ser Val Ile Pro Asn Val Thr Pro Leu Asp Lys Arg Ala
 625 630 635 640
 Gly Met Pro Asn Trp Gln Ile Ile His Ser Ala Glu Glu Val Gln Lys
 645 650 655
 Ala Leu Ala Glu Gly Arg Phe Ala Thr Pro Asp Gly Tyr Ile Phe Asp
 660 665 670
 Pro Arg Asp Val Leu Ala Lys Glu Thr Phe Val Trp Lys Asp Gly Ser
 675 680 685
 Phe Ser Ile Pro Arg Ala Asp Gly Ser Ser Leu Arg Thr Ile Asn Lys
 690 695 700
 Ser Asp Leu Ser Gln Ala Glu Trp Gln Gln Ala Gln Glu Leu Leu Ala
 705 710 715 720
 Lys Lys Asn Ala Gly Asp Ala Thr Asp Thr Asp Lys Pro Lys Glu Lys
 725 730 735
 Gln Gln Ala Asp Lys Ser Asn Glu Asn Gln Gln Pro Ser Glu Ala Ser
 740 745 750
 Lys Glu Glu Glu Lys Glu Ser Asp Asp Phe Ile Asp Ser Leu Pro Asp
 755 760 765
 Tyr Gly Leu Asp Arg Ala Thr Leu Glu Asp His Ile Asn Gln Leu Ala
 770 775 780
 Gln Lys Ala Asn Ile Asp Pro Lys Tyr Leu Ile Phe Gln Pro Glu Gly
 785 790 795 800
 Val Gln Phe Tyr Asn Lys Asn Gly Glu Leu Val Thr Tyr Asp Ile Lys
 805 810 815
 Thr Leu Gln Gln Ile Asn Pro Pro
 820

<210> 84
 <211> 1019
 <212> PRT
 <213> S. pneumoniae

<400> 84
 Cys Ala Tyr Ala Leu Asn Gln His Arg Ser Gln Glu Asn Lys Asp Asn
 1 5 10 15
 Asn Arg Val Ser Tyr Val Asp Gly Ser Gln Ser Ser Gln Lys Ser Glu
 20 25 30
 Asn Leu Thr Pro Asp Gln Val Ser Gln Lys Glu Gly Ile Gln Ala Glu
 35 40 45
 Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly
 50 55 60
 Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Leu Phe
 65 70 75 80
 Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp Ala
 85 90 95
 Asp Ile Val Asn Glu Val Lys Gly Gly Tyr Ile Ile Lys Val Asp Gly
 100 105 110

Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg
 115 120 125
 Thr Lys Asp Glu Ile Asn Arg Gln Lys Gln Glu His Val Lys Asp Asn
 130 135 140
 Glu Lys Val Asn Ser Asn Val Ala Val Ala Arg Ser Gln Gly Arg Tyr
 145 150 155 160
 Thr Thr Asn Asp Gly Tyr Val Phe Asn Pro Ala Asp Ile Ile Glu Asp
 165 170 175
 Thr Gly Asn Ala Tyr Ile Val Pro His Arg Gly His Tyr His Tyr Ile
 180 185 190
 Pro Lys Ser Asp Leu Ser Ala Ser Glu Leu Ala Ala Ala Lys Ala His
 195 200 205
 Leu Ala Gly Lys Asn Met Gln Pro Ser Gln Leu Ser Tyr Ser Ser Thr
 210 215 220
 Ala Ser Asp Asn Asn Thr Gln Ser Val Ala Lys Gly Ser Thr Ser Lys
 225 230 235 240
 Pro Ala Asn Lys Ser Glu Asn Leu Gln Ser Leu Leu Lys Glu Leu Tyr
 245 250 255
 Asp Ser Pro Ser Ala Gln Arg Tyr Ser Glu Ser Asp Gly Leu Val Phe
 260 265 270
 Asp Pro Ala Lys Ile Ile Ser Arg Thr Pro Asn Gly Val Ala Ile Pro
 275 280 285
 His Gly Asp His Tyr His Phe Ile Pro Tyr Ser Lys Leu Ser Ala Leu
 290 295 300
 Glu Glu Lys Ile Ala Arg Met Val Pro Ile Ser Gly Thr Gly Ser Thr
 305 310 315 320
 Val Ser Thr Asn Ala Lys Pro Asn Glu Val Val Ser Ser Leu Gly Ser
 325 330 335
 Leu Ser Ser Asn Pro Ser Ser Leu Thr Thr Ser Lys Glu Leu Ser Ser
 340 345 350
 Ala Ser Asp Gly Tyr Ile Phe Asn Pro Lys Asp Ile Val Glu Glu Thr
 355 360 365
 Ala Thr Ala Tyr Ile Val Arg His Gly Asp His Phe His Tyr Ile Pro
 370 375 380
 Lys Ser Asn Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala
 385 390 395 400
 Thr Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys
 405 410 415
 His Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu
 420 425 430
 Asp Glu Ser Gly Phe Val Met Ser His Gly Asp His Asn His Tyr Phe
 435 440 445
 Phe Lys Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His
 450 455 460
 Leu Glu Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser
 465 470 475 480
 His Glu Gln Asp Tyr Pro Ser Asn Ala Lys Glu Met Lys Asp Leu Asp
 485 490 495
 Lys Lys Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val
 500 505 510
 Lys Arg Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr
 515 520 525
 Pro His Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro
 530 535 540
 Val Gly Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu
 545 550 555 560

Glu Gly Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu
 565 570 575
 Leu Thr Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln
 580 585 590
 Asn Phe Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro
 595 600 605
 Pro Glu Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile
 610 615 620
 Thr Pro Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly
 625 630 635 640
 Glu Gly Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu
 645 650 655
 Pro Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu
 660 665 670
 Val Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys
 675 680 685
 Met Ala Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr
 690 695 700
 Leu Arg Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu
 705 710 715 720
 Val Arg Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn
 725 730 735
 Tyr Lys Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly
 740 745 750
 Thr Thr Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn
 755 760 765
 Ala Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu
 770 775 780
 Glu Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys
 785 790 795 800
 Arg Asn Lys Ala Gln Glu Asn Ser Lys Phe Asp Glu Lys Val Glu Glu
 805 810 815
 Pro Lys Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly
 820 825 830
 Asn Ser Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro
 835 840 845
 Val Gln Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu
 850 855 860
 Glu Asn Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro
 865 870 875 880
 Ser Gly Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala
 885 890 895
 Pro Gln Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser
 900 905 910
 Thr Gly Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser
 915 920 925
 Leu Pro Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr
 930 935 940
 Asp Asn Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met
 945 950 955 960
 Leu Asp Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu
 965 970 975
 Lys Leu Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val
 980 985 990
 Ile Phe Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu
 995 1000 1005

Val Ile Lys Lys Asn Leu Ser Asp Leu Ile Ala
1010 1015

<210> 85
<211> 1019
<212> PRT
<213> S. pneumoniae

<400> 85

Cys Ala Tyr Ala Leu Asn Gln His Arg Ser Gln Glu Asn Lys Asp Asn
1 5 10 15
Asn Arg Val Ser Tyr Val Asp Gly Ser Gln Ser Ser Gln Lys Ser Glu
20 25 30
Asn Leu Thr Pro Asp Gln Val Ser Gln Lys Glu Gly Ile Gln Ala Glu
35 40 45
Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly
50 55 60
Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Leu Phe
65 70 75 80
Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp Ala
85 90 95
Asp Ile Val Asn Glu Val Lys Gly Gly Tyr Ile Ile Lys Val Asp Gly
100 105 110
Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg
115 120 125
Thr Lys Asp Glu Ile Asn Arg Gln Lys Gln Glu His Val Lys Asp Asn
130 135 140
Glu Lys Val Asn Ser Asn Val Ala Val Ala Arg Ser Gln Gly Arg Tyr
145 150 155 160
Thr Thr Asn Asp Gly Tyr Val Phe Asn Pro Ala Asp Ile Ile Glu Asp
165 170 175
Thr Gly Asn Ala Tyr Ile Val Pro His Gly Gly His Tyr His Tyr Ile
180 185 190
Pro Lys Ser Asp Leu Ser Ala Ser Glu Leu Ala Ala Lys Ala His
195 200 205
Leu Ala Gly Lys Asn Met Gln Pro Ser Gln Leu Ser Tyr Ser Ser Thr
210 215 220
Ala Ser Asp Asn Asn Thr Gln Ser Val Ala Lys Gly Ser Thr Ser Lys
225 230 235 240
Pro Ala Asn Lys Ser Glu Asn Leu Gln Ser Leu Leu Lys Glu Leu Tyr
245 250 255
Asp Ser Pro Ser Ala Gln Arg Tyr Ser Glu Ser Asp Gly Leu Val Phe
260 265 270
Asp Pro Ala Lys Ile Ile Ser Arg Thr Pro Asn Gly Val Ala Ile Pro
275 280 285
His Gly Asp His Tyr His Phe Ile Pro Tyr Ser Lys Leu Ser Ala Leu
290 295 300
Glu Glu Lys Ile Ala Arg Arg Val Pro Ile Ser Gly Thr Gly Ser Thr
305 310 315 320
Val Ser Thr Asn Ala Lys Pro Asn Glu Val Val Ser Ser Leu Gly Ser
325 330 335
Leu Ser Ser Asn Pro Ser Ser Leu Thr Thr Ser Lys Glu Leu Ser Ser
340 345 350
Ala Ser Asp Gly Tyr Ile Phe Asn Pro Lys Asp Ile Val Glu Glu Thr
355 360 365
Ala Thr Ala Tyr Ile Val Arg His Gly Asp His Phe His Tyr Ile Pro
370 375 380

Lys Ser Asn Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala
 385 390 395 400
 Thr Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Ile Ser His Glu Lys
 405 410 415
 His Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu
 420 425 430
 Asp Glu Ser Gly Phe Ile Met Ser His Gly Asn His Asn His Tyr Phe
 435 440 445
 Phe Lys Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His
 450 455 460
 Leu Glu Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser
 465 470 475 480
 His Glu Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp
 485 490 495
 Lys Lys Ile Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val
 500 505 510
 Lys Arg Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr
 515 520 525
 Pro His Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro
 530 535 540
 Val Gly Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu
 545 550 555 560
 Glu Gly Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu
 565 570 575
 Leu Thr Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln
 580 585 590
 Asn Phe Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro
 595 600 605
 Pro Glu Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile
 610 615 620
 Thr Pro Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly
 625 630 635 640
 Glu Gly Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu
 645 650 655
 Pro Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu
 660 665 670
 Val Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys
 675 680 685
 Met Ala Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr
 690 695 700
 Leu Arg Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu
 705 710 715 720
 Val Arg Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn
 725 730 735
 Tyr Lys Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly
 740 745 750
 Thr Thr Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn
 755 760 765
 Ala Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu
 770 775 780
 Glu Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys
 785 790 795 800
 Arg Asn Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu
 805 810 815
 Pro Lys Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly
 820 825 830

Asn	Ser	Thr	Ser	Asn	Ser	Thr	Leu	Glu	Glu	Val	Pro	Thr	Val	Asp	Pro
		835					840					845			
Val	Gln	Glu	Lys	Val	Ala	Lys	Phe	Ala	Glu	Ser	Tyr	Gly	Met	Lys	Leu
	850					855					860				
Glu	Asn	Val	Leu	Phe	Asn	Met	Asp	Gly	Thr	Ile	Glu	Leu	Tyr	Leu	Pro
865					870					875					880
Ser	Gly	Glu	Val	Ile	Lys	Lys	Asn	Met	Ala	Asp	Phe	Thr	Gly	Glu	Ala
				885					890					895	
Pro	Gln	Gly	Asn	Gly	Glu	Asn	Lys	Pro	Ser	Glu	Asn	Gly	Lys	Val	Ser
			900					905					910		
Thr	Gly	Thr	Val	Glu	Asn	Gln	Pro	Thr	Glu	Asn	Lys	Pro	Ala	Asp	Ser
	915						920					925			
Leu	Pro	Glu	Ala	Pro	Asn	Glu	Lys	Pro	Val	Lys	Pro	Glu	Asn	Ser	Thr
	930					935					940				
Asp	Asn	Gly	Met	Leu	Asn	Pro	Glu	Gly	Asn	Val	Gly	Ser	Asp	Pro	Met
945					950					955					960
Leu	Asp	Pro	Ala	Leu	Glu	Glu	Ala	Pro	Ala	Val	Asp	Pro	Val	Gln	Glu
				965					970					975	
Lys	Leu	Glu	Lys	Phe	Thr	Ala	Ser	Tyr	Gly	Leu	Gly	Leu	Asp	Ser	Val
			980					985					990		
Ile	Phe	Asn	Met	Asp	Gly	Thr	Ile	Glu	Leu	Arg	Leu	Pro	Ser	Gly	Glu
	995						1000					1005			
Val	Ile	Lys	Lys	Asn	Leu	Ser	Asp	Leu	Ile	Ala					
	1010						1015								

<210> 86

<211> 1019

<212> PRT

<213> S. pneumoniae

<400> 86

Cys	Ala	Tyr	Ala	Leu	Asn	Gln	His	Arg	Ser	Gln	Glu	Asn	Lys	Asp	Asn
1				5					10					15	
Asn	Arg	Val	Ser	Tyr	Val	Asp	Gly	Ser	Gln	Ser	Ser	Gln	Lys	Ser	Glu
			20					25					30		
Asn	Leu	Thr	Pro	Asp	Gln	Val	Ser	Gln	Lys	Glu	Gly	Ile	Gln	Ala	Glu
		35					40					45			
Gln	Ile	Val	Ile	Lys	Ile	Thr	Asp	Gln	Gly	Tyr	Val	Thr	Ser	His	Gly
	50					55					60				
Asp	His	Tyr	His	Tyr	Tyr	Asn	Gly	Lys	Val	Pro	Tyr	Asp	Ala	Leu	Phe
65					70					75					80
Ser	Glu	Glu	Leu	Leu	Met	Lys	Asp	Pro	Asn	Tyr	Gln	Leu	Lys	Asp	Ala
				85					90					95	
Asp	Ile	Val	Asn	Glu	Val	Lys	Gly	Gly	Tyr	Ile	Ile	Lys	Val	Asp	Gly
			100					105					110		
Lys	Tyr	Tyr	Val	Tyr	Leu	Lys	Asp	Ala	Ala	His	Ala	Asp	Asn	Val	Arg
		115					120					125			
Thr	Lys	Asp	Glu	Ile	Asn	Arg	Gln	Lys	Gln	Glu	His	Val	Lys	Asp	Asn
	130					135					140				
Glu	Lys	Val	Asn	Ser	Asn	Val	Ala	Val	Ala	Arg	Ser	Gln	Gly	Arg	Tyr
145					150					155					160
Thr	Thr	Asn	Asp	Gly	Tyr	Val	Phe	Asn	Pro	Ala	Asp	Ile	Ile	Glu	Asp
				165					170					175	
Thr	Gly	Asn	Ala	Tyr	Ile	Val	Pro	His	Gly	Gly	His	Tyr	His	Tyr	Ile
			180					185					190		
Pro	Lys	Ser	Asp	Leu	Ser	Ala	Ser	Glu	Leu	Ala	Ala	Ala	Lys	Ala	His
		195					200					205			

Leu Ala Gly Lys Asn Met Gln Pro Ser Gln Leu Ser Tyr Ser Ser Thr
 210 215 220
 Ala Ser Asp Asn Asn Thr Gln Ser Val Ala Lys Gly Ser Thr Ser Lys
 225 230 235 240
 Pro Ala Asn Lys Ser Glu Asn Leu Gln Ser Leu Leu Lys Glu Leu Tyr
 245 250 255
 Asp Ser Pro Ser Ala Gln Arg Tyr Ser Glu Ser Asp Gly Leu Val Phe
 260 265 270
 Asp Pro Ala Lys Ile Ile Ser Arg Thr Pro Asn Gly Val Ala Ile Pro
 275 280 285
 His Gly Asp His Tyr His Phe Ile Pro Tyr Ser Lys Leu Ser Ala Leu
 290 295 300
 Glu Glu Lys Ile Ala Arg Met Val Pro Ile Ser Gly Thr Gly Ser Thr
 305 310 315 320
 Val Ser Thr Asn Ala Lys Pro Asn Glu Val Val Ser Ser Leu Gly Ser
 325 330 335
 Leu Ser Ser Asn Pro Ser Ser Leu Thr Thr Ser Lys Glu Leu Ser Ser
 340 345 350
 Ala Ser Asp Gly Tyr Ile Phe Asn Pro Lys Asp Ile Val Glu Glu Thr
 355 360 365
 Ala Thr Ala Tyr Ile Val Arg His Gly Asp His Phe His Tyr Ile Pro
 370 375 380
 Lys Ser Asn Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala
 385 390 395 400
 Thr Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys
 405 410 415
 His Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu
 420 425 430
 Asp Glu Ser Gly Phe Val Met Ser His Gly Asp His Asn His Tyr Phe
 435 440 445
 Phe Lys Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His
 450 455 460
 Leu Glu Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser
 465 470 475 480
 His Glu Gln Asp Tyr Pro Ser Asn Ala Lys Glu Met Lys Asp Leu Asp
 485 490 495
 Lys Lys Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val
 500 505 510
 Lys Arg Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr
 515 520 525
 Pro His Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro
 530 535 540
 Val Gly Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu
 545 550 555 560
 Glu Gly Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu
 565 570 575
 Leu Thr Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln
 580 585 590
 Asn Phe Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro
 595 600 605
 Pro Glu Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile
 610 615 620
 Thr Pro Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly
 625 630 635 640
 Glu Gly Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu
 645 650 655

Pro Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu
 660 665 670
 Val Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys
 675 680 685
 Met Ala Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr
 690 695 700
 Leu Arg Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu
 705 710 715 720
 Val Arg Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn
 725 730 735
 Tyr Lys Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly
 740 745 750
 Thr Thr Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn
 755 760 765
 Ala Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu
 770 775 780
 Glu Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys
 785 790 795 800
 Arg Asn Lys Ala Gln Glu Asn Leu Lys Leu Asp Glu Lys Val Glu Glu
 805 810 815
 Pro Lys Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly
 820 825 830
 Asn Ser Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro
 835 840 845
 Val Gln Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu
 850 855 860
 Glu Asn Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro
 865 870 875 880
 Ser Gly Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala
 885 890 895
 Pro Gln Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser
 900 905 910
 Thr Gly Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser
 915 920 925
 Leu Pro Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr
 930 935 940
 Asp Asn Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met
 945 950 955 960
 Leu Asp Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu
 965 970 975
 Lys Leu Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val
 980 985 990
 Ile Phe Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu
 995 1000 1005
 Val Ile Lys Lys Asn Leu Ser Asp Leu Ile Ala
 1010 1015

<210> 87
 <211> 1019
 <212> PRT
 <213> S. pneumoniae

<400> 87
 Cys Ala Tyr Ala Leu Asn Gln His Arg Ser Gln Glu Asn Lys Asp Asn
 1 5 10 15
 Asn Arg Val Ser Tyr Val Asp Gly Ser Gln Ser Ser Gln Lys Ser Glu
 20 25 30

Asn Leu Thr Pro Asp Gln Val Ser Gln Lys Glu Gly Ile Gln Ala Glu
 35 40 45
 Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly
 50 55 60
 Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Leu Phe
 65 70 75 80
 Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp Ala
 85 90 95
 Asp Ile Val Asn Glu Val Lys Gly Gly Tyr Ile Ile Lys Val Asp Gly
 100 105 110
 Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg
 115 120 125
 Thr Lys Asp Glu Ile Asn Arg Gln Lys Gln Glu His Val Lys Asp Asn
 130 135 140
 Glu Lys Val Asn Ser Asn Val Ala Val Ala Arg Ser Gln Gly Arg Tyr
 145 150 155 160
 Thr Thr Asn Asp Gly Tyr Val Phe Asn Pro Ala Asp Ile Ile Glu Asp
 165 170 175
 Thr Gly Asn Ala Tyr Ile Val Pro His Gly Gly His Tyr His Tyr Ile
 180 185 190
 Pro Lys Ser Asp Leu Ser Ala Ser Glu Leu Ala Ala Ala Lys Ala His
 195 200 205
 Leu Ala Gly Lys Asn Met Gln Pro Ser Gln Leu Ser Tyr Ser Ser Thr
 210 215 220
 Ala Ser Asp Asn Asn Thr Gln Ser Val Ala Lys Gly Ser Thr Ser Lys
 225 230 235 240
 Pro Ala Asn Lys Ser Glu Asn Leu Gln Ser Leu Leu Lys Glu Leu Tyr
 245 250 255
 Asp Ser Pro Ser Ala Gln Arg Tyr Ser Glu Ser Asp Gly Leu Val Phe
 260 265 270
 Asp Pro Ala Lys Ile Ile Ser Arg Thr Pro Asn Gly Val Ala Ile Pro
 275 280 285
 His Gly Asp His Tyr His Phe Ile Pro Tyr Ser Lys Leu Ser Ala Leu
 290 295 300
 Glu Glu Lys Ile Ala Arg Met Val Pro Ile Ser Gly Thr Gly Ser Thr
 305 310 315 320
 Val Ser Thr Asn Ala Lys Pro Asn Glu Val Val Ser Ser Leu Gly Ser
 325 330 335
 Leu Ser Ser Asn Pro Ser Ser Leu Thr Thr Ser Lys Glu Leu Ser Ser
 340 345 350
 Ala Ser Asp Gly Tyr Ile Phe Asn Pro Lys Asp Ile Val Glu Glu Thr
 355 360 365
 Ala Thr Ala Tyr Ile Val Arg His Gly Asp His Phe His Tyr Ile Pro
 370 375 380
 Lys Ser Asn Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala
 385 390 395 400
 Thr Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys
 405 410 415
 His Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu
 420 425 430
 Asp Glu Ser Gly Phe Val Met Ser His Gly Asp His Asn His Tyr Phe
 435 440 445
 Phe Lys Lys Asp Leu Thr Glu Gln Ile Lys Ala Ala Gln Lys His
 450 455 460
 Leu Glu Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser
 465 470 475 480

His Glu Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp
 485 490 495
 Lys Lys Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val
 500 505 510
 Lys Arg Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr
 515 520 525
 Pro His Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro
 530 535 540
 Val Gly Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu
 545 550 555 560
 Glu Gly Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu
 565 570 575
 Leu Thr Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln
 580 585 590
 Asn Phe Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro
 595 600 605
 Pro Glu Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile
 610 615 620
 Thr Pro Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly
 625 630 635 640
 Glu Gly Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu
 645 650 655
 Pro Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu
 660 665 670
 Val Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys
 675 680 685
 Met Ala Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr
 690 695 700
 Leu Arg Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu
 705 710 715 720
 Val Arg Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn
 725 730 735
 Tyr Lys Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly
 740 745 750
 Thr Thr Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn
 755 760 765
 Ala Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu
 770 775 780
 Glu Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys
 785 790 795 800
 Arg Asn Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu
 805 810 815
 Pro Lys Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly
 820 825 830
 Asn Ser Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro
 835 840 845
 Val Gln Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu
 850 855 860
 Glu Asn Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro
 865 870 875 880
 Ser Gly Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala
 885 890 895
 Pro Gln Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser
 900 905 910
 Thr Gly Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser
 915 920 925

Leu Pro Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr
 930 935 940
 Asp Asn Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met
 945 950 955 960
 Leu Asp Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu
 965 970 975
 Lys Leu Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val
 980 985 990
 Ile Phe Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu
 995 1000 1005
 Val Ile Lys Lys Asn Leu Ser Asp Phe Ile Ala
 1010 1015

<210> 88
 <211> 1019
 <212> PRT
 <213> S. pneumoniae

<400> 88
 Cys Ala Tyr Ala Leu Asn Gln His Arg Ser Gln Glu Asn Lys Asp Asn
 1 5 10 15
 Asn Arg Val Ser Tyr Val Asp Gly Ser Gln Ser Ser Gln Lys Ser Glu
 20 25 30
 Asn Leu Thr Pro Asp Gln Val Ser Gln Lys Glu Gly Ile Gln Ala Glu
 35 40 45
 Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly
 50 55 60
 Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Leu Phe
 65 70 75 80
 Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp Ala
 85 90 95
 Asp Ile Val Asn Glu Val Lys Gly Gly Tyr Ile Ile Lys Val Asp Gly
 100 105 110
 Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg
 115 120 125
 Thr Lys Asp Glu Ile Asn Arg Gln Lys Glu His Val Lys Asp Asn
 130 135 140
 Glu Lys Val Asn Ser Asn Val Ala Val Ala Arg Ser Gln Gly Arg Tyr
 145 150 155 160
 Thr Thr Asn Asp Gly Tyr Val Phe Asn Pro Ala Asp Ile Ile Glu Asp
 165 170 175
 Thr Gly Asn Ala Tyr Ile Val Pro His Arg Gly His Tyr His Tyr Ile
 180 185 190
 Pro Lys Ser Asp Leu Ser Ala Ser Glu Leu Ala Ala Ala Lys Ala His
 195 200 205
 Leu Ala Gly Lys Asn Met Gln Pro Ser Gln Leu Ser Tyr Ser Ser Thr
 210 215 220
 Ala Ser Asp Asn Asn Thr Gln Ser Val Ala Lys Gly Ser Thr Ser Lys
 225 230 235 240
 Pro Ala Asn Lys Ser Glu Asn Leu Gln Ser Leu Leu Lys Glu Leu Tyr
 245 250 255
 Asp Ser Pro Ser Ala Gln Arg Tyr Ser Glu Ser Asp Gly Leu Val Phe
 260 265 270
 Asp Pro Ala Lys Ile Ile Ser Arg Thr Pro Asn Gly Val Ala Ile Pro
 275 280 285
 His Gly Asp His Tyr His Phe Ile Pro Tyr Ser Lys Leu Ser Ala Leu
 290 295 300

Glu Glu Lys Ile Ala Arg Met Val Pro Ile Ser Gly Thr Gly Ser Thr
 305 310 315 320
 Val Ser Thr Asn Ala Lys Pro Asn Glu Val Val Ser Ser Leu Gly Ser
 325 330 335
 Leu Ser Ser Asn Pro Ser Ser Leu Thr Thr Ser Lys Glu Leu Ser Ser
 340 345 350
 Ala Ser Asp Gly Tyr Ile Phe Asn Pro Lys Asp Ile Val Glu Glu Thr
 355 360 365
 Ala Thr Ala Tyr Ile Val Arg His Gly Asp His Phe His Tyr Ile Pro
 370 375 380
 Lys Ser Asn Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala
 385 390 395 400
 Thr Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys
 405 410 415
 His Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu
 420 425 430
 Asp Glu Ser Gly Phe Val Met Ser His Gly Asp His Asn His Tyr Phe
 435 440 445
 Phe Lys Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His
 450 455 460
 Leu Glu Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser
 465 470 475 480
 His Glu Gln Asp Tyr Pro Ser Asn Ala Lys Glu Met Lys Asp Leu Asp
 485 490 495
 Lys Lys Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val
 500 505 510
 Lys Arg Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr
 515 520 525
 Pro His Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro
 530 535 540
 Val Gly Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu
 545 550 555 560
 Glu Gly Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu
 565 570 575
 Leu Thr Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln
 580 585 590
 Asn Phe Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro
 595 600 605
 Pro Glu Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile
 610 615 620
 Thr Pro Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly
 625 630 635 640
 Glu Gly Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu
 645 650 655
 Pro Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu
 660 665 670
 Val Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys
 675 680 685
 Met Ala Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr
 690 695 700
 Leu Arg Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu
 705 710 715 720
 Val Arg Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn
 725 730 735
 Tyr Lys Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly
 740 745 750

Thr Thr Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn
 755 760 765
 Ala Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu
 770 775 780
 Glu Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys
 785 790 795 800
 Arg Asn Lys Ala Gln Glu Asn Ser Lys Phe Asp Glu Lys Val Glu Glu
 805 810 815
 Pro Lys Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly
 820 825 830
 Asn Ser Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro
 835 840 845
 Val Gln Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu
 850 855 860
 Glu Asn Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro
 865 870 875 880
 Ser Gly Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala
 885 890 895
 Pro Gln Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser
 900 905 910
 Thr Gly Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser
 915 920 925
 Leu Pro Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr
 930 935 940
 Asp Asn Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met
 945 950 955 960
 Leu Asp Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu
 965 970 975
 Lys Leu Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val
 980 985 990
 Ile Phe Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu
 995 1000 1005
 Val Ile Lys Lys Asn Leu Ser Asp Leu Ile Ala
 1010 1015

<210> 89

<211> 1019

<212> PRT

<213> S. pneumoniae

<400> 89

Cys Ala Tyr Ala Leu Asn Gln His Arg Ser Gln Glu Asn Lys Asp Asn
 1 5 10 15
 Asn Arg Val Ser Tyr Val Asp Gly Ser Gln Ser Ser Gln Lys Ser Glu
 20 25 30
 Asn Leu Thr Pro Asp Gln Val Ser Gln Lys Glu Gly Ile Gln Ala Glu
 35 40 45
 Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly
 50 55 60
 Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Leu Phe
 65 70 75 80
 Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp Ala
 85 90 95
 Asp Ile Val Asn Glu Val Lys Gly Gly Tyr Ile Ile Lys Val Asp Gly
 100 105 110
 Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg
 115 120 125

Thr	Lys	Asp	Glu	Ile	Asn	Arg	Gln	Lys	Gln	Glu	His	Val	Lys	Asp	Asn	130	135	140
Glu	Lys	Val	Asn	Ser	Asn	Val	Ala	Val	Ala	Arg	Ser	Gln	Gly	Arg	Tyr	145	150	155
Thr	Thr	Asn	Asp	Gly	Tyr	Val	Phe	Asn	Pro	Ala	Asp	Ile	Ile	Glu	Asp	165	170	175
Thr	Gly	Asn	Ala	Tyr	Ile	Val	Pro	His	Arg	Gly	His	Tyr	His	Tyr	Ile	180	185	190
Pro	Lys	Ser	Asp	Leu	Ser	Ala	Ser	Glu	Leu	Ala	Ala	Ala	Lys	Ala	His	195	200	205
Leu	Ala	Gly	Lys	Asn	Met	Gln	Pro	Ser	Gln	Leu	Ser	Tyr	Ser	Ser	Thr	210	215	220
Ala	Ser	Asp	Asn	Asn	Thr	Gln	Ser	Val	Ala	Lys	Gly	Ser	Thr	Ser	Lys	225	230	235
Pro	Ala	Asn	Lys	Ser	Glu	Asn	Leu	Gln	Ser	Leu	Leu	Lys	Glu	Leu	Tyr	245	250	255
Asp	Ser	Pro	Ser	Ala	Gln	Arg	Tyr	Ser	Glu	Ser	Asp	Gly	Leu	Val	Phe	260	265	270
Asp	Pro	Ala	Lys	Ile	Ile	Ser	Arg	Thr	Pro	Asn	Gly	Val	Ala	Ile	Pro	275	280	285
His	Gly	Asp	His	Tyr	His	Phe	Ile	Pro	Tyr	Ser	Lys	Leu	Ser	Ala	Leu	290	295	300
Glu	Glu	Lys	Ile	Ala	Arg	Met	Val	Pro	Ile	Ser	Gly	Thr	Gly	Ser	Thr	305	310	315
Val	Ser	Thr	Asn	Ala	Lys	Pro	Asn	Glu	Val	Val	Ser	Ser	Leu	Gly	Ser	325	330	335
Leu	Ser	Ser	Asn	Pro	Ser	Ser	Leu	Thr	Thr	Ser	Lys	Glu	Leu	Ser	Ser	340	345	350
Ala	Ser	Asp	Gly	Tyr	Ile	Phe	Asn	Pro	Lys	Asp	Ile	Val	Glu	Glu	Thr	355	360	365
Ala	Thr	Ala	Tyr	Ile	Val	Arg	His	Gly	Asp	His	Phe	His	Tyr	Ile	Pro	370	375	380
Lys	Ser	Asn	Gln	Ile	Gly	Gln	Pro	Thr	Leu	Pro	Asn	Asn	Ser	Leu	Ala	385	390	395
Thr	Pro	Ser	Pro	Ser	Leu	Pro	Ile	Asn	Pro	Gly	Thr	Ser	His	Glu	Lys	405	410	415
His	Glu	Glu	Asp	Gly	Tyr	Gly	Phe	Asp	Ala	Asn	Arg	Ile	Ile	Ala	Glu	420	425	430
Asp	Glu	Ser	Gly	Phe	Val	Met	Ser	His	Gly	Asp	His	Asn	His	Tyr	Phe	435	440	445
Phe	Lys	Lys	Asp	Leu	Thr	Glu	Glu	Gln	Ile	Lys	Ala	Ala	Gln	Lys	His	450	455	460
Leu	Glu	Glu	Val	Lys	Thr	Ser	His	Asn	Gly	Leu	Asp	Ser	Leu	Ser	Ser	465	470	475
His	Glu	Gln	Asp	Tyr	Pro	Ser	Asn	Ala	Lys	Glu	Met	Lys	Asp	Leu	Asp	485	490	495
Lys	Lys	Ile	Glu	Glu	Lys	Ile	Ala	Gly	Ile	Met	Lys	Gln	Tyr	Gly	Val	500	505	510
Lys	Arg	Glu	Ser	Ile	Val	Val	Asn	Lys	Glu	Lys	Asn	Ala	Ile	Ile	Tyr	515	520	525
Pro	His	Gly	Asp	His	His	His	Ala	Asp	Pro	Ile	Asp	Glu	His	Lys	Pro	530	535	540
Val	Gly	Ile	Gly	His	Ser	His	Ser	Asn	Tyr	Glu	Leu	Phe	Lys	Pro	Glu	545	550	555
Glu	Gly	Val	Ala	Lys	Lys	Glu	Gly	Asn	Lys	Val	Tyr	Thr	Gly	Glu	Glu	565	570	575

Leu	Thr	Asn	Val	Val	Asn	Leu	Leu	Lys	Asn	Ser	Thr	Phe	Asn	Asn	Gln
			580					585					590		
Asn	Phe	Thr	Leu	Ala	Asn	Gly	Gln	Lys	Arg	Val	Ser	Phe	Ser	Phe	Pro
		595					600					605			
Pro	Glu	Leu	Glu	Lys	Lys	Leu	Gly	Ile	Asn	Met	Leu	Val	Lys	Leu	Ile
	610					615					620				
Thr	Pro	Asp	Gly	Lys	Val	Leu	Glu	Lys	Val	Ser	Gly	Lys	Val	Phe	Gly
625					630					635					640
Glu	Gly	Val	Gly	Asn	Ile	Ala	Asn	Phe	Glu	Leu	Asp	Gln	Pro	Tyr	Leu
			645					650						655	
Pro	Gly	Gln	Thr	Phe	Lys	Tyr	Thr	Ile	Ala	Ser	Lys	Asp	Tyr	Pro	Glu
			660					665					670		
Val	Ser	Tyr	Asp	Gly	Thr	Phe	Thr	Val	Pro	Thr	Ser	Leu	Ala	Tyr	Lys
		675					680					685			
Met	Ala	Ser	Gln	Thr	Ile	Phe	Tyr	Pro	Phe	His	Ala	Gly	Asp	Thr	Tyr
		690				695					700				
Leu	Arg	Val	Asn	Pro	Gln	Phe	Ala	Val	Pro	Lys	Gly	Thr	Asp	Ala	Leu
705					710					715					720
Val	Arg	Val	Phe	Asp	Glu	Phe	His	Gly	Asn	Ala	Tyr	Leu	Glu	Asn	Asn
			725					730						735	
Tyr	Lys	Val	Gly	Glu	Ile	Lys	Leu	Pro	Ile	Pro	Lys	Leu	Asn	Gln	Gly
			740					745					750		
Thr	Thr	Arg	Thr	Ala	Gly	Asn	Lys	Ile	Pro	Val	Thr	Phe	Met	Ala	Asn
		755					760					765			
Ala	Tyr	Leu	Asp	Asn	Gln	Ser	Thr	Tyr	Ile	Val	Glu	Val	Pro	Ile	Leu
		770				775					780				
Glu	Lys	Glu	Asn	Gln	Thr	Asp	Lys	Pro	Ser	Ile	Leu	Pro	Gln	Phe	Lys
785					790					795					800
Arg	Asn	Lys	Ala	Gln	Glu	Asn	Ser	Lys	Phe	Asp	Glu	Lys	Val	Glu	Glu
			805						810					815	
Pro	Lys	Thr	Ser	Glu	Lys	Val	Glu	Lys	Glu	Lys	Leu	Ser	Glu	Thr	Gly
			820					825					830		
Asn	Ser	Thr	Ser	Asn	Ser	Thr	Leu	Glu	Glu	Val	Pro	Thr	Val	Asp	Pro
		835					840					845			
Val	Gln	Glu	Lys	Val	Ala	Lys	Phe	Ala	Glu	Ser	Tyr	Gly	Met	Lys	Leu
		850				855					860				
Glu	Asn	Val	Leu	Phe	Asn	Met	Asp	Gly	Thr	Ile	Glu	Leu	Tyr	Leu	Pro
865					870					875					880
Ser	Gly	Glu	Val	Ile	Lys	Lys	Asn	Met	Ala	Asp	Phe	Thr	Gly	Glu	Ala
			885						890					895	
Pro	Gln	Gly	Asn	Gly	Glu	Asn	Lys	Pro	Ser	Glu	Asn	Gly	Lys	Val	Ser
			900					905					910		
Thr	Gly	Thr	Val	Glu	Asn	Gln	Pro	Thr	Glu	Asn	Lys	Pro	Ala	Asp	Ser
		915					920					925			
Leu	Pro	Glu	Ala												

<210> 90
 <211> 819
 <212> PRT
 <213> S. pneumoniae

<400> 90

Cys Ser Tyr Glu Leu Gly Arg His Gln Ala Gly Gln Val Lys Lys Glu
 1 5 10 15
 Ser Asn Arg Val Ser Tyr Ile Asp Gly Asp Gln Ala Gly Gln Lys Ala
 20 25 30
 Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala
 35 40 45
 Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His
 50 55 60
 Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile
 65 70 75 80
 Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp
 85 90 95
 Ser Asp Ile Val Asn Glu Ile Lys Gly Tyr Val Ile Lys Val Asp
 100 105 110
 Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Ile
 115 120 125
 Arg Thr Lys Glu Glu Ile Lys Arg Gln Lys Gln Glu His Ser His Asn
 130 135 140
 His Asn Ser Arg Ala Asp Asn Ala Val Ala Ala Ala Arg Ala Gln Gly
 145 150 155 160
 Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser Asp Ile Ile
 165 170 175
 Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asp His Tyr His
 180 185 190
 Tyr Ile Pro Lys Asn Glu Leu Ser Ala Ser Glu Leu Ala Ala Ala Glu
 195 200 205
 Ala Tyr Trp Asn Gly Lys Gln Gly Ser Arg Pro Ser Ser Ser Ser Ser
 210 215 220
 Tyr Asn Ala Asn Pro Val Gln Pro Arg Leu Ser Glu Asn His Asn Leu
 225 230 235 240
 Thr Val Thr Pro Thr Tyr His Gln Asn Gln Gly Glu Asn Ile Ser Ser
 245 250 255
 Leu Leu Arg Glu Leu Tyr Ala Lys Pro Leu Ser Glu Arg His Val Glu
 260 265 270
 Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr Ala
 275 280 285
 Arg Gly Val Ala Val Pro His Gly Asn His Tyr His Phe Ile Pro Tyr
 290 295 300
 Glu Gln Met Ser Glu Leu Glu Lys Arg Ile Ala Arg Ile Ile Pro Leu
 305 310 315 320
 Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Gln Pro
 325 330 335
 Ser Pro Gln Ser Thr Pro Glu Pro Ser Pro Ser Leu Gln Pro Ala Pro
 340 345 350
 Asn Pro Gln Pro Ala Pro Ser Asn Pro Ile Asp Glu Lys Leu Val Lys
 355 360 365
 Glu Ala Val Arg Lys Val Gly Asp Gly Tyr Val Phe Glu Glu Asn Gly
 370 375 380
 Val Ser Arg Tyr Ile Pro Ala Lys Asp Leu Ser Ala Glu Thr Ala Ala
 385 390 395 400

Gly Ile Asp Ser Lys Leu Ala Lys Gln Glu Ser Leu Ser His Lys Leu
 405 410 415
 Gly Ala Lys Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu Phe Tyr Asn
 420 425 430
 Lys Ala Tyr Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp Asn
 435 440 445
 Lys Gly Arg Gln Val Asp Phe Glu Val Leu Asp Asn Leu Leu Glu Arg
 450 455 460
 Leu Lys Asp Val Ser Ser Asp Lys Val Lys Leu Val Asp Asp Ile Leu
 465 470 475 480
 Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro Asn
 485 490 495
 Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
 500 505 510
 Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp Ile
 515 520 525
 Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His Ser
 530 535 540
 His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala
 545 550 555 560
 Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His
 565 570 575
 Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn
 580 585 590
 Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn
 595 600 605
 Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His
 610 615 620
 Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu
 625 630 635 640
 Tyr Glu Ala Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val
 645 650 655
 Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn Gly
 660 665 670
 Phe Gly Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp Gln Asp
 675 680 685
 Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu Pro Thr
 690 695 700
 His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn Pro Ser
 705 710 715 720
 Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr Glu Glu
 725 730 735
 Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gln Val Glu Asn
 740 745 750
 Ser Val Ile Asn Ala Lys Ile Ala Asp Ala Glu Ala Leu Leu Glu Lys
 755 760 765
 Val Thr Asp Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly
 770 775 780
 Leu Lys Ser Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser
 785 790 795 800
 Ala Glu Val Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala
 805 810 815
 Pro Ile Gln


<210> 91

<211> 820

<212> PRT

<213> S. pneumoniae

<400> 91



Cys	Ser	Tyr	Glu	Leu	Gly	Arg	His	Gln	Ala	Gly	Gln	Val	Lys	Lys	Glu
1				5					10					15	
Ser	Asn	Arg	Val	Ser	Tyr	Ile	Asp	Gly	Asp	Gln	Ala	Gly	Gln	Lys	Ala
			20					25					30		
Glu	Asn	Leu	Thr	Pro	Asp	Glu	Val	Ser	Lys	Arg	Glu	Gly	Ile	Asn	Ala
		35					40					45			
Glu	Gln	Ile	Val	Ile	Lys	Ile	Thr	Asp	Gln	Gly	Tyr	Val	Thr	Ser	His
	50					55					60				
Gly	Asp	His	Tyr	His	Tyr	Tyr	Asn	Gly	Lys	Val	Pro	Tyr	Asp	Ala	Ile
65					70					75					80
Ile	Ser	Glu	Glu	Leu	Leu	Met	Lys	Asp	Pro	Asn	Tyr	Gln	Leu	Lys	Asp
				85					90					95	
Ser	Asp	Ile	Val	Asn	Glu	Ile	Lys	Gly	Gly	Tyr	Val	Ile	Lys	Val	Asp
			100					105					110		
Gly	Lys	Tyr	Tyr	Val	Tyr	Leu	Lys	Asp	Ala	Ala	His	Ala	Asp	Asn	Ile
		115					120					125			
Arg	Thr	Lys	Glu	Glu	Ile	Lys	Arg	Gln	Lys	Gln	Glu	His	Ser	His	Asn
	130					135					140				
His	Gly	Gly	Gly	Ser	Asn	Asp	Gln	Ala	Val	Val	Ala	Ala	Arg	Ala	Gln
145					150					155					160
Gly	Arg	Tyr	Thr	Thr	Asp	Asp	Gly	Tyr	Ile	Phe	Asn	Ala	Ser	Asp	Ile
			165					170						175	
Ile	Glu	Asp	Thr	Gly	Asp	Ala	Tyr	Ile	Val	Pro	His	Gly	Asp	His	Tyr
		180						185					190		
His	Tyr	Ile	Pro	Lys	Asn	Glu	Leu	Ser	Ala	Ser	Glu	Leu	Ala	Ala	Ala
	195						200					205			
Glu	Ala	Tyr	Trp	Asn	Gly	Lys	Gln	Gly	Ser	Arg	Pro	Ser	Ser	Ser	Ser
	210				215						220				
Ser	Tyr	Asn	Ala	Asn	Pro	Ala	Gln	Pro	Arg	Leu	Ser	Glu	Asn	His	Asn
225					230					235					240
Leu	Thr	Val	Thr	Pro	Thr	Tyr	His	Gln	Asn	Gln	Gly	Glu	Asn	Ile	Ser
			245					250						255	
Ser	Leu	Leu	Arg	Glu	Leu	Tyr	Ala	Lys	Pro	Leu	Ser	Glu	Arg	His	Val
			260					265					270		
Glu	Ser	Asp	Gly	Leu	Ile	Phe	Asp	Pro	Ala	Gln	Ile	Thr	Ser	Arg	Thr
		275					280					285			
Ala	Arg	Gly	Val	Ala	Val	Pro	His	Gly	Asn	His	Tyr	His	Phe	Ile	Pro
	290					295					300				
Tyr	Glu	Gln	Met	Ser	Glu	Leu	Glu	Lys	Arg	Ile	Ala	Arg	Ile	Ile	Pro
305					310					315					320
Leu	Arg	Tyr	Arg	Ser	Asn	His	Trp	Val	Pro	Asp	Ser	Arg	Pro	Glu	Gln
			325						330					335	
Pro	Ser	Pro	Gln	Ser	Thr	Pro	Glu	Pro	Ser	Pro	Ser	Pro	Gln	Pro	Ala
		340						345					350		
Pro	Asn	Pro	Gln	Pro	Ala	Pro	Ser	Asn	Pro	Ile	Asp	Glu	Lys	Leu	Val
	355						360					365			
Lys	Glu	Ala	Val	Arg	Lys	Val	Gly	Asp	Gly	Tyr	Val	Phe	Glu	Glu	Asn
	370					375					380				
Gly	Val	Ser	Arg	Tyr	Ile	Pro	Ala	Lys	Asp	Leu	Ser	Ala	Glu	Thr	Ala
385					390					395					400
Ala	Gly	Ile	Asp	Ser	Lys	Leu	Ala	Lys	Gln	Glu	Ser	Leu	Ser	His	Lys
				405					410					415	

Leu Gly Ala Lys Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu Phe Tyr
 420 425 430
 Asn Lys Ala Tyr Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp
 435 440 445
 Asn Lys Gly Arg Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu
 450 455 460
 Arg Leu Lys Asp Val Pro Ser Asp Lys Val Lys Leu Val Asp Asp Ile
 465 470 475 480
 Leu Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro
 485 490 495
 Asn Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu
 500 505 510
 Ala Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp
 515 520 525
 Ile Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His
 530 535 540
 Ser His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala
 545 550 555 560
 Ala Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp
 565 570 575
 His Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr
 580 585 590
 Asn Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr
 595 600 605
 Asn Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro
 610 615 620
 His Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly
 625 630 635 640
 Leu Tyr Glu Ala Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu Ala Thr
 645 650 655
 Val Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn
 660 665 670
 Gly Phe Gly Asn Ala Ser Asp His Val Arg Lys Asn Lys Val Asp Gln
 675 680 685
 Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu Pro
 690 695 700
 Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn Pro
 705 710 715 720
 Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr Glu
 725 730 735
 Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gln Val Glu
 740 745 750
 Asn Ser Val Ile Asn Ala Lys Ile Ala Asp Ala Glu Ala Leu Leu Glu
 755 760 765
 Lys Val Thr Asp Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr
 770 775 780
 Gly Leu Lys Ser Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile
 785 790 795 800
 Ser Ala Glu Val Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro
 805 810 815
 Ala Pro Ile Gln
 820

<210> 92

<211> 816

<212> PRT

<213> S. pneumoniae

<400> 92

Cys	Ser	Tyr	Glu	Leu	Gly	Arg	His	Gln	Ala	Gly	Gln	Asp	Lys	Lys	Glu
1				5					10					15	
Ser	Asn	Arg	Val	Ala	Tyr	Ile	Asp	Gly	Asp	Gln	Ala	Gly	Gln	Lys	Ala
			20					25					30		
Glu	Asn	Leu	Thr	Pro	Asp	Glu	Val	Ser	Lys	Arg	Glu	Gly	Ile	Asn	Ala
		35					40					45			
Glu	Gln	Ile	Val	Ile	Lys	Ile	Thr	Asp	Gln	Gly	Tyr	Val	Thr	Ser	His
		50				55					60				
Gly	Asp	His	Tyr	His	Tyr	Tyr	Asn	Gly	Lys	Val	Pro	Tyr	Asp	Ala	Ile
65					70					75					80
Ile	Ser	Glu	Glu	Leu	Leu	Met	Lys	Asp	Pro	Asn	Tyr	Gln	Leu	Lys	Asp
				85					90					95	
Ser	Asp	Ile	Val	Asn	Glu	Ile	Lys	Gly	Gly	Tyr	Val	Ile	Lys	Val	Asn
			100					105					110		
Gly	Lys	Tyr	Tyr	Val	Tyr	Leu	Lys	Asp	Ala	Ala	His	Ala	Asp	Asn	Ile
		115					120					125			
Arg	Thr	Lys	Glu	Glu	Ile	Lys	Arg	Gln	Lys	Gln	Glu	His	Ser	His	Asn
	130					135					140				
His	Gly	Gly	Gly	Ser	Asn	Asp	Gln	Ala	Val	Val	Ala	Ala	Arg	Ala	Gln
145					150					155					160
Gly	Arg	Tyr	Thr	Thr	Asp	Asp	Gly	Tyr	Ile	Phe	Asn	Ala	Ser	Asp	Ile
			165					170						175	
Ile	Glu	Asp	Thr	Gly	Asp	Ala	Tyr	Ile	Val	Pro	His	Gly	Asn	His	Phe
			180					185					190		
His	Tyr	Ile	Pro	Lys	Ser	Asp	Leu	Ser	Ala	Ser	Glu	Leu	Ala	Ala	Ala
		195					200					205			
Gln	Ala	Tyr	Trp	Asn	Gly	Lys	Gln	Gly	Ser	Arg	Pro	Ser	Ser	Ser	Ser
	210					215					220				
Ser	His	Asn	Ala	Asn	Pro	Ala	Gln	Pro	Arg	Leu	Ser	Glu	Asn	His	Asn
225					230					235					240
Leu	Thr	Val	Thr	Pro	Thr	Tyr	His	Gln	Asn	Gln	Gly	Glu	Asn	Ile	Ser
			245						250					255	
Ser	Leu	Leu	Arg	Glu	Leu	Tyr	Ala	Lys	Pro	Leu	Ser	Glu	Arg	His	Val
			260					265					270		
Glu	Ser	Asp	Gly	Leu	Ile	Phe	Asp	Pro	Ala	Gln	Ile	Thr	Ser	Arg	Thr
		275					280					285			
Ala	Arg	Gly	Val	Ala	Val	Pro	His	Gly	Asn	His	Tyr	His	Phe	Ile	Pro
	290					295					300				
Tyr	Glu	Gln	Met	Ser	Glu	Leu	Glu	Glu	Arg	Ile	Ala	Arg	Ile	Ile	Pro
305					310					315					320
Leu	Arg	Tyr	Arg	Ser	Asn	His	Trp	Val	Pro	Asp	Ser	Arg	Pro	Glu	Gln
			325						330					335	
Pro	Ser	Pro	Gln	Pro	Ser	Pro	Ser	Pro	Gln	Pro	Ala	Pro	Asn	Pro	Gln
			340					345					350		
Pro	Ala	Pro	Ser	Asn	Pro	Ile	Asp	Glu	Lys	Leu	Val	Lys	Glu	Ala	Val
		355					360					365			
Arg	Lys	Val	Gly	Asp	Gly	Tyr	Val	Phe	Glu	Glu	Asn	Gly	Val	Ser	Arg
	370					375					380				
Tyr	Ile	Pro	Ala	Lys	Asp	Leu	Ser	Ala	Glu	Thr	Ala	Ala	Gly	Ile	Asp
385					390					395					400
Ser	Lys	Leu	Ala	Lys	Gln	Glu	Ser	Leu	Ser	His	Lys	Leu	Gly	Thr	Lys
			405						410					415	
Lys	Thr	Asp	Leu	Pro	Ser	Ser	Asp	Arg	Glu	Phe	Tyr	Asn	Lys	Ala	Tyr
			420					425						430	

Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp Asn Lys Gly Arg
 435 440 445
 Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu Arg Leu Lys Asp
 450 455 460
 Val Ser Ser Asp Lys Val Lys Leu Val Glu Asp Ile Leu Ala Phe Leu
 465 470 475 480
 Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro Asn Ser Gln Ile
 485 490 495
 Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala Gly Lys Tyr
 500 505 510
 Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp Ile Thr Ser Asp
 515 520 525
 Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His Ser His Trp Ile
 530 535 540
 Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Gln Ala Tyr
 545 550 555 560
 Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Arg Asp Ser
 565 570 575
 Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
 580 585 590
 Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
 595 600 605
 Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His Tyr Asp His
 610 615 620
 Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
 625 630 635 640
 Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
 645 650 655
 Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn Gly Phe Gly Asn
 660 665 670
 Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp Gln Asp Ser Lys Pro
 675 680 685
 Asp Glu Asp Lys Gly His Asp Glu Val Ser Glu Pro Thr His Pro Glu
 690 695 700
 Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn Pro Ser Ala Asp Asn
 705 710 715 720
 Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr Glu Glu Glu Ala Glu
 725 730 735
 Asp Thr Thr Asp Glu Ala Glu Ile Pro Gln Val Glu His Ser Val Ile
 740 745 750
 Asn Ala Lys Ile Ala Asp Ala Glu Ala Leu Leu Glu Lys Val Thr Asp
 755 760 765
 Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
 770 775 780
 Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
 785 790 795 800
 Asp Ser Leu Leu Ala Leu Leu Lys Lys Ser Gln Pro Ala Pro Ile Gln
 805 810 815

<210> 93
 <211> 816
 <212> PRT
 <213> S. pneumoniae

<400> 93
 Cys Ser Tyr Glu Leu Gly Arg His Gln Ala Gly Gln Asp Lys Lys Glu
 1 5 10 15

Ser Asn Arg Val Ala Tyr Ile Asp Gly Asp Gln Ala Gly Gln Lys Ala
 20 25 30
 Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala
 35 40 45
 Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His
 50 55 60
 Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile
 65 70 75 80
 Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp
 85 90 95
 Ser Asp Ile Val Asn Glu Ile Lys Gly Gly Tyr Val Ile Lys Val Asn
 100 105 110
 Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Ile
 115 120 125
 Arg Thr Lys Glu Glu Ile Lys Arg Gln Arg Gln Glu His Ser His Asn
 130 135 140
 His Gly Gly Gly Ser Asn Asp Gln Ala Val Val Ala Ala Arg Ala Gln
 145 150 155 160
 Gly Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser Asp Ile
 165 170 175
 Ile Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asn His Phe
 180 185 190
 His Tyr Ile Pro Lys Ser Asp Leu Ser Ala Ser Glu Leu Ala Ala Ala
 195 200 205
 Gln Ala Tyr Trp Asn Gly Lys Gln Gly Ser Arg Pro Ser Ser Ser Ser
 210 215 220
 Ser His Asn Ala Asn Pro Ala Gln Pro Arg Leu Ser Glu Asn His Asn
 225 230 235 240
 Leu Thr Val Thr Pro Thr Tyr His Gln Asn Gln Gly Glu Asn Ile Ser
 245 250 255
 Ser Leu Leu Arg Glu Leu Tyr Ala Lys Pro Leu Ser Glu Arg His Val
 260 265 270
 Glu Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr
 275 280 285
 Ala Arg Gly Val Ala Val Pro His Gly Asn His Tyr His Phe Ile Pro
 290 295 300
 Tyr Glu Gln Met Ser Glu Leu Glu Glu Arg Ile Ala Arg Ile Ile Pro
 305 310 315 320
 Leu Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Gln
 325 330 335
 Pro Ser Pro Gln Pro Ser Pro Ser Pro Gln Pro Ala Pro Asn Pro Gln
 340 345 350
 Pro Ala Pro Ser Asn Pro Ile Asp Glu Lys Leu Val Lys Glu Ala Val
 355 360 365
 Arg Lys Val Gly Asp Gly Tyr Val Phe Glu Glu Asn Gly Val Ser Arg
 370 375 380
 Tyr Ile Pro Ala Lys Asp Leu Ser Ala Glu Thr Ala Ala Gly Ile Asp
 385 390 395 400
 Ser Lys Leu Ala Lys Gln Glu Ser Leu Ser His Lys Leu Gly Thr Lys
 405 410 415
 Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu Phe Tyr Asn Lys Ala Tyr
 420 425 430
 Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp Asn Lys Gly Arg
 435 440 445
 Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu Arg Leu Lys Asp
 450 455 460

Val Ser Ser Asp Lys Val Lys Leu Val Glu Asp Ile Leu Ala Phe Leu
 465 470 475 480
 Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro Asn Ser Gln Ile
 485 490 495
 Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala Gly Lys Tyr
 500 505 510
 Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp Ile Thr Ser Asp
 515 520 525
 Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His Ser His Trp Ile
 530 535 540
 Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
 545 550 555 560
 Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
 565 570 575
 Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
 580 585 590
 Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
 595 600 605
 Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His Tyr Asp His
 610 615 620
 Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
 625 630 635 640
 Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
 645 650 655
 Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn Gly Phe Gly Asn
 660 665 670
 Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp Gln Asp Ser Lys Pro
 675 680 685
 Asp Glu Asp Lys Gly His Asp Glu Val Ser Glu Pro Thr His Pro Glu
 690 695 700
 Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn Pro Ser Ala Asp Asn
 705 710 715 720
 Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr Glu Glu Ala Glu
 725 730 735
 Asp Thr Thr Asp Glu Ala Glu Ile Pro Gln Val Glu His Ser Val Ile
 740 745 750
 Asn Ala Lys Ile Ala Asp Ala Glu Ala Leu Leu Glu Lys Val Thr Asp
 755 760 765
 Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
 770 775 780
 Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
 785 790 795 800
 Asp Ser Leu Leu Ala Leu Leu Lys Lys Ser Gln Pro Ala Pro Ile Gln
 805 810 815

<210> 94
 <211> 816
 <212> PRT
 <213> S. pneumoniae

<400> 94
 Cys Ser Tyr Glu Leu Gly Arg His Gln Ala Gly Gln Asp Lys Lys Glu
 1 5 10 15
 Ser Asn Arg Val Ala Tyr Ile Asp Gly Asp Gln Ala Gly Gln Lys Ala
 20 25 30
 Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala
 35 40 45

Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His
 50 55 60
 Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile
 65 70 75 80
 Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp
 85 90 95
 Ser Asp Ile Val Asn Glu Ile Lys Gly Gly Tyr Val Ile Lys Val Asn
 100 105 110
 Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Ile
 115 120 125
 Arg Thr Lys Glu Glu Ile Lys Arg Gln Lys Gln Glu His Ser His Asn
 130 135 140
 His Gly Gly Gly Ser Asn Asp Gln Ala Val Val Ala Ala Arg Ala Gln
 145 150 155 160
 Gly Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser Asp Ile
 165 170 175
 Ile Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro Arg Gly Asn His Phe
 180 185 190
 His Tyr Ile Pro Lys Ser Asp Leu Ser Ala Ser Glu Leu Ala Ala Ala
 195 200 205
 Gln Ala Tyr Trp Asn Gly Lys Gln Gly Ser Arg Pro Ser Ser Ser Ser
 210 215 220
 Ser His Asn Ala Asn Pro Ala Gln Pro Arg Leu Ser Glu Asn His Asn
 225 230 235 240
 Leu Thr Val Thr Pro Thr Tyr His Gln Asn Gln Gly Glu Asn Ile Ser
 245 250 255
 Ser Leu Leu Arg Glu Leu Tyr Ala Lys Pro Leu Ser Glu Arg Arg Val
 260 265 270
 Glu Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr
 275 280 285
 Ala Arg Gly Val Ala Val Pro His Gly Asn His Tyr His Phe Ile Pro
 290 295 300
 Tyr Glu Gln Met Ser Glu Leu Glu Glu Arg Ile Ala Arg Ile Ile Pro
 305 310 315 320
 Leu Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Gln
 325 330 335
 Pro Ser Pro Gln Pro Ser Pro Ser Pro Gln Pro Ala Pro Asn Pro Gln
 340 345 350
 Pro Ala Pro Ser Asn Pro Ile Asp Glu Lys Leu Val Lys Glu Ala Val
 355 360 365
 Arg Lys Val Gly Asp Gly Tyr Val Phe Glu Glu Asn Gly Val Ser Arg
 370 375 380
 Tyr Ile Pro Ala Lys Asp Leu Ser Ala Glu Thr Ala Ala Gly Ile Asp
 385 390 395 400
 Ser Lys Leu Ala Lys Gln Glu Ser Leu Ser His Lys Leu Gly Thr Lys
 405 410 415
 Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu Phe Tyr Asn Lys Ala Tyr
 420 425 430
 Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp Asn Lys Gly Arg
 435 440 445
 Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu Arg Leu Lys Asp
 450 455 460
 Val Ser Ser Asp Lys Val Lys Leu Val Glu Asp Ile Leu Ala Phe Leu
 465 470 475 480
 Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro Asn Ser Gln Ile
 485 490 495

Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala Gly Lys Tyr
 500 505 510
 Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp Ile Thr Ser Asp
 515 520 525
 Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His Ser His Trp Ile
 530 535 540
 Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
 545 550 555 560
 Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
 565 570 575
 Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
 580 585 590
 Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
 595 600 605
 Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His Tyr Asp His
 610 615 620
 Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
 625 630 635 640
 Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
 645 650 655
 Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn Gly Phe Gly Asn
 660 665 670
 Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp Gln Asp Ser Lys Pro
 675 680 685
 Asp Glu Asp Lys Gly His Asp Glu Val Ser Glu Pro Thr His Pro Glu
 690 695 700
 Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn Pro Ser Ala Asp Asn
 705 710 715 720
 Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr Glu Glu Glu Ala Glu
 725 730 735
 Asp Thr Thr Asp Glu Ala Glu Ile Pro Gln Val Glu His Ser Val Ile
 740 745 750
 Asn Ala Lys Ile Ala Asp Ala Glu Ala Leu Leu Glu Lys Val Thr Asp
 755 760 765
 Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
 770 775 780
 Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
 785 790 795 800
 Asp Ser Leu Leu Ala Leu Leu Lys Lys Ser Gln Pro Ala Pro Ile Gln
 805 810 815

<210> 95
 <211> 834
 <212> PRT
 <213> S. pneumoniae

<400> 95
 Cys Ser Tyr Glu Leu Gly Arg His Gln Ala Gly Gln Val Lys Lys Glu
 1 5 10 15
 Ser Asn Arg Val Ser Tyr Ile Asp Gly Asp Gln Ala Gly Gln Lys Ala
 20 25 30
 Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala
 35 40 45
 Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His
 50 55 60
 Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile
 65 70 75 80

Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp
 85 90 95
 Ser Asp Ile Val Asn Glu Ile Lys Gly Gly Tyr Val Ile Lys Val Asp
 100 105 110
 Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Ile
 115 120 125
 Arg Thr Lys Glu Glu Ile Lys Arg Gln Lys Gln Glu Arg Ser His Asn
 130 135 140
 His Asn Ser Arg Ala Asp Asn Ala Val Ala Ala Ala Arg Ala Gln Gly
 145 150 155 160
 Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser Asp Ile Ile
 165 170 175
 Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asp His Tyr His
 180 185 190
 Tyr Ile Pro Lys Ser Asp Leu Ser Ala Ser Glu Leu Ala Ala Ala Gln
 195 200 205
 Ala Tyr Trp Asn Gly Lys Gln Gly Ser Arg Pro Ser Ser Ser Ser
 210 215 220
 His Asn Ala Asn Pro Ala Gln Pro Arg Leu Ser Glu Asn His Asn Leu
 225 230 235 240
 Thr Val Thr Pro Thr Tyr His Gln Asn Gln Gly Glu Asn Ile Ser Ser
 245 250 255
 Leu Leu Arg Glu Leu Tyr Ala Lys Pro Leu Ser Glu Arg His Val Glu
 260 265 270
 Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr Ala
 275 280 285
 Asn Gly Val Ala Val Pro His Gly Asp His Tyr His Phe Ile Pro Tyr
 290 295 300
 Ser Gln Leu Ser Pro Leu Glu Glu Lys Leu Ala Arg Ile Ile Pro Leu
 305 310 315 320
 Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Gln Pro
 325 330 335
 Ser Pro Gln Ser Thr Pro Glu Pro Ser Pro Ser Pro Gln Pro Ala Pro
 340 345 350
 Asn Pro Gln Pro Ala Pro Ser Asn Pro Ile Asp Glu Lys Leu Val Lys
 355 360 365
 Glu Ala Val Arg Lys Val Gly Asp Gly Tyr Val Phe Glu Glu Asn Gly
 370 375 380
 Val Pro Arg Tyr Ile Pro Ala Lys Asp Leu Ser Ala Glu Thr Ala Ala
 385 390 395 400
 Gly Ile Asp Ser Lys Leu Ala Lys Gln Glu Ser Leu Ser His Lys Leu
 405 410 415
 Gly Ala Lys Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu Phe Tyr Asn
 420 425 430
 Lys Ala Tyr Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp Asn
 435 440 445
 Lys Gly Arg Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu Arg
 450 455 460
 Leu Lys Asp Val Ser Ser Asp Lys Val Lys Leu Val Asp Asp Ile Leu
 465 470 475 480
 Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro Asn
 485 490 495
 Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
 500 505 510
 Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp Ile
 515 520 525

Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His Ser
 530 535 540
 His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala
 545 550 555 560
 Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His
 565 570 575
 Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn
 580 585 590
 Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn
 595 600 605
 Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His
 610 615 620
 Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu
 625 630 635 640
 Tyr Glu Ala Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val
 645 650 655
 Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn Gly
 660 665 670
 Phe Gly Asn Ala Ser Asp His Val Gln Arg Asn Lys Asn Gly Gln Ala
 675 680 685
 Asp Thr Asn Gln Thr Glu Lys Pro Asn Glu Glu Lys Pro Gln Thr Glu
 690 695 700
 Lys Pro Glu Glu Asp Lys Glu His Asp Glu Val Ser Glu Pro Thr His
 705 710 715 720
 Pro Glu Ser Asp Glu Lys Glu Asn His Val Gly Leu Asn Pro Ser Ala
 725 730 735
 Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr Glu Glu Glu
 740 745 750
 Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gln Val Glu Tyr Ser
 755 760 765
 Val Ile Asn Ala Lys Ile Ala Glu Ala Glu Ala Leu Leu Glu Lys Val
 770 775 780
 Thr Asp Ser Ser Ile Arg Gln Asn Ala Val Glu Thr Leu Thr Gly Leu
 785 790 795 800
 Lys Ser Ser Leu Leu Glu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala
 805 810 815
 Glu Val Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro
 820 825 830
 Ile Gln

<210> 96
 <211> 811
 <212> PRT
 <213> S. pneumoniae

<400> 96
 Cys Ser Tyr Glu Leu Gly Arg His Gln Ala Gly Gln Asp Lys Lys Glu
 1 5 10 15
 Ser Asn Arg Val Ala Tyr Ile Asp Gly Asp Gln Ala Gly Gln Lys Ala
 20 25 30
 Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala
 35 40 45
 Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His
 50 55 60
 Gly Asp His Tyr His Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile
 65 70 75 80

Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp
 85 90 95
 Ser Asp Ile Val Asn Glu Ile Lys Gly Gly Tyr Val Ile Lys Val Asn
 100 105 110
 Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Ile
 115 120 125
 Arg Thr Lys Glu Glu Ile Lys Arg Gln Lys Gln Glu His Ser His Asn
 130 135 140
 His Gly Gly Gly Ser Asn Asp Gln Ala Val Val Ala Ala Arg Ala Gln
 145 150 155 160
 Gly Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser Asp Ile
 165 170 175
 Ile Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asn His Phe
 180 185 190
 His Tyr Ile Pro Lys Ser Asp Leu Ser Ala Ser Glu Leu Ala Ala Ala
 195 200 205
 Gln Ala Tyr Trp Asn Gly Lys Gln Gly Ser Arg Pro Ser Ser Ser Ser
 210 215 220
 Ser His Asn Ala Asn Pro Ala Gln Pro Arg Leu Ser Glu Asn His Asn
 225 230 235 240
 Leu Thr Val Thr Pro Thr Tyr His Gln Asn Gln Gly Glu Asn Ile Ser
 245 250 255
 Ser Leu Leu Arg Glu Leu Tyr Ala Lys Pro Leu Ser Glu Arg His Val
 260 265 270
 Glu Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr
 275 280 285
 Ala Arg Gly Val Ala Val Pro His Gly Asn His Tyr His Phe Ile Pro
 290 295 300
 Tyr Glu Gln Met Ser Glu Leu Glu Glu Arg Ile Ala Arg Ile Ile Pro
 305 310 315 320
 Leu Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Gln
 325 330 335
 Pro Ser Pro Gln Pro Ser Pro Ser Pro Gln Pro Ala Pro Asn Pro Gln
 340 345 350
 Pro Ala Pro Ser Asn Pro Ile Asp Glu Lys Leu Val Lys Glu Ala Val
 355 360 365
 Arg Lys Val Gly Asp Gly Tyr Val Phe Glu Glu Asn Gly Val Ser Arg
 370 375 380
 Tyr Ile Pro Ala Lys Asp Leu Ser Ala Glu Thr Ala Ala Gly Ile Asp
 385 390 395 400
 Ser Lys Leu Ala Lys Gln Glu Ser Leu Ser His Lys Leu Gly Thr Lys
 405 410 415
 Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu Phe Tyr Asn Lys Ala Tyr
 420 425 430
 Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp Asn Lys Gly Arg
 435 440 445
 Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu Arg Leu Lys Asp
 450 455 460
 Val Ser Ser Asp Lys Val Lys Leu Val Glu Asp Ile Leu Ala Phe Leu
 465 470 475 480
 Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro Asn Ser Gln Ile
 485 490 495
 Thr Tyr Thr Asp Glu Ile Gln Val Ala Lys Leu Ala Gly Lys Tyr
 500 505 510
 Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp Ile Thr Ser Asp
 515 520 525

Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His Ser His Trp Ile
 530 535 540
 Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
 545 550 555 560
 Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
 565 570 575
 Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
 580 585 590
 Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
 595 600 605
 Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His Tyr Asp His
 610 615 620
 Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
 625 630 635 640
 Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
 645 650 655
 Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn Gly Phe Gly Asn
 660 665 670
 Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp Gln Asp Ser Lys Pro
 675 680 685
 Asp Glu Asp Lys Gly His Asp Glu Val Ser Glu Pro Thr His Pro Glu
 690 695 700
 Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn Pro Ser Ala Asp Asn
 705 710 715 720
 Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr Glu Glu Glu Ala Glu
 725 730 735
 Asp Thr Thr Asp Glu Ala Glu Ile Pro Gln Val Glu His Ser Val Ile
 740 745 750
 Asn Ala Lys Ile Ala Asp Ala Glu Ala Leu Leu Glu Lys Val Thr Asp
 755 760 765
 Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
 770 775 780
 Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
 785 790 795 800
 Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Lys
 805 810

<210> 97
 <211> 811
 <212> PRT
 <213> S. pneumoniae

<400> 97
 Cys Ser Tyr Glu Leu Gly Arg His Gln Ala Gly Gln Asp Lys Lys Glu
 1 5 10 15
 Ser Asn Arg Val Ala Tyr Ile Asp Gly Asp Gln Ala Gly Gln Lys Ala
 20 25 30
 Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala
 35 40 45
 Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His
 50 55 60
 Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile
 65 70 75 80
 Ile Ser Glu Glu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp
 85 90 95
 Ser Asp Ile Val Asn Glu Ile Lys Gly Gly Tyr Val Ile Lys Val Asn
 100 105 110

Gly Lys Tyr Tyr Gly Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Ile
 115 120 125
 Arg Thr Lys Glu Glu Ile Lys Arg Gln Lys Gln Glu His Ser His Asn
 130 135 140
 His Gly Gly Gly Ser Asn Asp Gln Ala Val Val Ala Ala Arg Ala Gln
 145 150 155 160
 Gly Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser Asp Ile
 165 170 175
 Ile Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asn His Phe
 180 185 190
 His Tyr Ile Pro Lys Ser Asp Leu Ser Ala Ser Glu Leu Ala Ala Ala
 195 200 205
 Gln Ala Tyr Trp Asn Gly Lys Gln Gly Ser Arg Pro Ser Ser Ser Ser
 210 215 220
 Ser His Asn Ala Asn Pro Ala Gln Pro Arg Leu Ser Glu Asn His Asn
 225 230 235 240
 Leu Thr Val Thr Pro Thr Tyr His Gln Asn Gln Gly Glu Asn Ile Ser
 245 250 255
 Ser Leu Leu Arg Glu Leu Tyr Ala Lys Pro Leu Ser Glu Arg His Val
 260 265 270
 Glu Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr
 275 280 285
 Ala Arg Gly Val Ala Val Pro His Gly Asn His Tyr His Phe Ile Pro
 290 295 300
 Tyr Glu Gln Met Ser Glu Leu Glu Glu Arg Ile Ala Arg Ile Ile Pro
 305 310 315 320
 Leu Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Gln
 325 330 335
 Pro Ser Pro Gln Pro Ser Pro Ser Pro Gln Pro Ala Pro Asn Pro Gln
 340 345 350
 Pro Ala Pro Ser Asn Pro Ile Asp Glu Lys Leu Val Lys Glu Ala Val
 355 360 365
 Arg Lys Val Gly Asp Gly Tyr Val Phe Glu Glu Asn Gly Val Ser Arg
 370 375 380
 Tyr Ile Pro Ala Lys Asp Leu Ser Ala Glu Thr Ala Ala Gly Ile Asp
 385 390 395 400
 Ser Lys Leu Ala Lys Gln Glu Ser Leu Ser His Lys Leu Gly Thr Lys
 405 410 415
 Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu Phe Tyr Asn Lys Ala Tyr
 420 425 430
 Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp Asn Lys Gly Arg
 435 440 445
 Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu Arg Leu Lys Asp
 450 455 460
 Val Ser Ser Asp Lys Val Lys Leu Val Glu Asp Ile Leu Ala Phe Leu
 465 470 475 480
 Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro Asn Ser Gln Ile
 485 490 495
 Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala Gly Lys Tyr
 500 505 510
 Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp Ile Thr Ser Asp
 515 520 525
 Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His Ser His Trp Ile
 530 535 540
 Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
 545 550 555 560

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
565 570 575
Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
580 585 590
Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
595 600 605
Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His Tyr Asp His
610 615 620
Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
625 630 635 640
Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
645 650 655
Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn Gly Phe Gly Asn
660 665 670
Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp Gln Asp Ser Lys Pro
675 680 685
Asp Glu Asp Lys Gly His Asp Glu Val Ser Glu Pro Thr His Pro Glu
690 695 700
Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn Pro Ser Ala Asp Asn
705 710 715 720
Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr Glu Glu Glu Ala Glu
725 730 735
Asp Thr Thr Asp Glu Ala Glu Ile Pro Gln Val Glu His Ser Val Ile
740 745 750
Asn Ala Lys Ile Ala Asp Ala Glu Ala Leu Leu Glu Lys Val Thr Asp
755 760 765
Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
770 775 780
Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
785 790 795 800
Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Lys
805 810

<210> 98

<211> 811

<212> PRT

<213> S. pneumoniae

<400> 98

Cys Ser Tyr Glu Leu Gly Arg His Gln Ala Gly Gln Asp Lys Lys Glu
1 5 10 15
Ser Asn Arg Val Ala Tyr Ile Asp Gly Asp Gln Ala Gly Gln Lys Ala
20 25 30
Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala
35 40 45
Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His
50 55 60
Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile
65 70 75 80
Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp
85 90 95
Ser Asp Ile Val Asn Glu Ile Lys Gly Tyr Val Ile Lys Val Asn
100 105 110
Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Ile
115 120 125
Arg Thr Lys Glu Glu Ile Lys Arg Gln Lys Gln Glu His Ser His Asn
130 135 140

His Gly Gly Gly Ser Asn Asp Gln Ala Val Val Ala Ala Arg Ala Gln
 145 150 155 160
 Gly Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser Asp Ile
 165 170 175
 Ile Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asn His Phe
 180 185 190
 His Tyr Ile Pro Lys Ser Asp Leu Ser Ala Ser Glu Leu Ala Ala Ala
 195 200 205
 Gln Ala Tyr Trp Asn Gly Lys Gln Gly Ser Arg Pro Ser Ser Ser Ser
 210 215 220
 Ser His Asn Ala Asn Pro Ala Gln Pro Arg Leu Ser Glu Asn His Asn
 225 230 235 240
 Leu Thr Val Thr Pro Thr Tyr His Gln Asn Gln Gly Glu Asn Ile Ser
 245 250 255
 Ser Leu Leu Arg Glu Leu Tyr Ala Lys Pro Leu Ser Glu Arg His Val
 260 265 270
 Glu Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr
 275 280 285
 Ala Arg Gly Val Ala Val Pro His Gly Asn His Tyr His Phe Ile Pro
 290 295 300
 Tyr Glu Gln Met Ser Glu Leu Glu Glu Arg Ile Ala Arg Ile Ile Pro
 305 310 315 320
 Leu Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Gln
 325 330 335
 Pro Ser Pro Gln Pro Ser Pro Ser Pro Gln Pro Ala Pro Asn Pro Gln
 340 345 350
 Pro Ala Pro Ser Asn Pro Ile Asp Glu Lys Leu Val Lys Glu Ala Val
 355 360 365
 Arg Lys Val Gly Asp Gly Tyr Val Phe Glu Glu Asn Gly Val Ser Arg
 370 375 380
 Tyr Ile Pro Ala Lys Asp Leu Ser Ala Glu Thr Ala Ala Gly Ile Asp
 385 390 395 400
 Ser Lys Leu Ala Lys Gln Glu Ser Leu Ser His Lys Leu Gly Thr Lys
 405 410 415
 Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu Phe Tyr Asn Lys Ala Tyr
 420 425 430
 Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp Asn Lys Gly Arg
 435 440 445
 Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu Arg Leu Lys Asp
 450 455 460
 Val Ser Ser Asp Lys Val Lys Leu Val Glu Asp Ile Leu Ala Phe Leu
 465 470 475 480
 Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro Asn Ser Gln Ile
 485 490 495
 Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala Gly Lys Tyr
 500 505 510
 Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp Ile Thr Ser Asp
 515 520 525
 Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His Ser His Trp Ile
 530 535 540
 Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
 545 550 555 560
 Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
 565 570 575
 Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
 580 585 590

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
 595 600 605
 Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His Tyr Asp His
 610 615 620
 Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
 625 630 635 640
 Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
 645 650 655
 Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn Gly Phe Gly Asn
 660 665 670
 Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp Gln Asp Ser Lys Pro
 675 680 685
 Asp Glu Asp Lys Gly His Asp Glu Val Ser Glu Pro Thr His Pro Glu
 690 695 700
 Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn Pro Ser Ala Asp Asn
 705 710 715 720
 Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr Glu Glu Ala Glu
 725 730 735
 Asp Thr Thr Asp Glu Ala Glu Ile Pro Gln Val Glu His Ser Val Ile
 740 745 750
 Asn Ala Lys Ile Ala Asp Ala Glu Ala Leu Leu Glu Lys Val Thr Asp
 755 760 765
 Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
 770 775 780
 Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
 785 790 795 800
 Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Lys
 805 810

<210> 99
 <211> 811
 <212> PRT
 <213> S. pneumoniae

<400> 99

Cys Ser Tyr Glu Leu Gly Arg His Gln Ala Gly Gln Val Lys Lys Glu
 1 5 10 15
 Ser Asn Arg Val Ser Tyr Ile Asp Gly Asp Gln Ala Gly Gln Lys Ala
 20 25 30
 Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala
 35 40 45
 Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His
 50 55 60
 Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile
 65 70 75 80
 Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp
 85 90 95
 Ser Asp Ile Val Asn Glu Ile Lys Gly Gly Tyr Val Ile Lys Val Asp
 100 105 110
 Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Ile
 115 120 125
 Arg Thr Lys Glu Glu Ile Lys Arg Gln Lys Gln Glu Arg Ser His Asn
 130 135 140
 His Asn Ser Arg Ala Asp Asn Ala Val Ala Ala Arg Ala Gln Gly
 145 150 155 160
 Arg Tyr Thr Thr Asp Gly Tyr Ile Phe Asn Ala Ser Asp Ile Ile
 165 170 175

Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asp His Tyr His
 180 185 190
 Tyr Ile Pro Lys Ser Asp Leu Ser Ala Ser Glu Leu Ala Ala Gln
 195 200 205
 Ala Tyr Trp Asn Gly Lys Gln Gly Ser Arg Pro Ser Ser Ser Ser Ser
 210 215 220
 His Asn Ala Asn Pro Ala Gln Pro Arg Leu Ser Glu Asn His Asn Leu
 225 230 235 240
 Thr Val Thr Pro Thr Tyr His Gln Asn Gln Gly Glu Asn Ile Ser Ser
 245 250 255
 Leu Leu Arg Glu Leu Tyr Ala Lys Pro Leu Ser Glu Arg His Val Glu
 260 265 270
 Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr Ala
 275 280 285
 Asn Gly Val Ala Val Pro His Gly Asp His Tyr His Phe Ile Pro Tyr
 290 295 300
 Ser Gln Leu Ser Pro Leu Glu Glu Lys Leu Ala Arg Ile Ile Pro Leu
 305 310 315 320
 Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Gln Pro
 325 330 335
 Ser Pro Gln Ser Thr Pro Glu Pro Ser Pro Ser Pro Gln Pro Ala Pro
 340 345 350
 Asn Pro Gln Pro Ala Pro Ser Asn Pro Ile Asp Glu Lys Leu Val Lys
 355 360 365
 Glu Ala Val Arg Lys Val Gly Asp Gly Tyr Val Phe Glu Glu Asn Gly
 370 375 380
 Val Pro Arg Tyr Ile Pro Ala Lys Asp Leu Ser Ala Glu Thr Ala Ala
 385 390 395 400
 Gly Ile Asp Ser Lys Leu Ala Lys Gln Glu Ser Leu Ser His Lys Leu
 405 410 415
 Gly Ala Lys Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu Phe Tyr Asn
 420 425 430
 Lys Ala Tyr Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp Asn
 435 440 445
 Lys Gly Arg Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu Arg
 450 455 460
 Leu Lys Asp Val Ser Ser Asp Lys Val Lys Leu Val Asp Asp Ile Leu
 465 470 475 480
 Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro Asn
 485 490 495
 Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
 500 505 510
 Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp Ile
 515 520 525
 Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His Ser
 530 535 540
 His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala
 545 550 555 560
 Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His
 565 570 575
 Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn
 580 585 590
 Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn
 595 600 605
 Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His
 610 615 620

Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu
 625 630 635 640
 Tyr Glu Ala Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val
 645 650 655
 Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn Gly
 660 665 670
 Phe Gly Asn Ala Ser Asp His Val Gln Arg Asn Lys Asn Gly Gln Ala
 675 680 685
 Asp Thr Asn Gln Thr Glu Lys Pro Asn Glu Glu Lys Pro Gln Thr Glu
 690 695 700
 Lys Pro Glu Glu Glu Thr Pro Arg Glu Glu Lys Pro Gln Ser Glu Lys
 705 710 715 720
 Pro Glu Ser Pro Lys Pro Thr Glu Glu Pro Glu Glu Glu Ser Pro Glu
 725 730 735
 Glu Ser Pro Glu Glu Ser Glu Glu Pro Gln Val Glu Thr Glu Lys Val
 740 745 750
 Lys Glu Lys Leu Arg Glu Ala Glu Asp Leu Leu Gly Lys Ile Gln Asn
 755 760 765
 Pro Ile Ile Lys Ser Asn Ala Lys Glu Thr Leu Thr Gly Leu Lys Asn
 770 775 780
 Asn Leu Leu Phe Gly Thr Gln Asp Asn Asn Thr Ile Met Ala Glu Ala
 785 790 795 800
 Glu Lys Leu Leu Ala Leu Leu Lys Glu Ser Lys
 805 810

<210> 100

<211> 805

<212> PRT

<213> S. pneumoniae

<400> 100

Cys Ser Tyr Glu Leu Gly Arg His Gln Ala Gly Gln Asp Lys Lys Glu
 1 5 10 15
 Ser Asn Arg Val Ala Tyr Ile Asp Gly Asp Gln Ala Gly Gln Lys Ala
 20 25 30
 Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala
 35 40 45
 Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His
 50 55 60
 Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile
 65 70 75 80
 Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp
 85 90 95
 Ser Asp Ile Val Asn Glu Ile Lys Gly Gly Tyr Val Ile Lys Val Asn
 100 105 110
 Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Ile
 115 120 125
 Arg Thr Lys Glu Glu Ile Lys Arg Gln Lys Gln Glu Arg Ser His Asn
 130 135 140
 His Asn Ser Arg Ala Asp Asn Ala Val Ala Ala Ala Arg Ala Gln Gly
 145 150 155 160
 Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser Asp Ile Ile
 165 170 175
 Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asp His Tyr His
 180 185 190
 Tyr Ile Pro Lys Asn Glu Leu Ser Ala Ser Glu Leu Ala Ala Glu
 195 200 205

Ala	Tyr	Trp	Asn	Gly	Lys	Gln	Gly	Ser	Arg	Pro	Ser	Ser	Ser	Ser	Ser	210	215	220
Tyr	Asn	Ala	Asn	Pro	Ala	Gln	Pro	Arg	Leu	Ser	Glu	Asn	His	Asn	Leu	225	230	235
Thr	Val	Thr	Pro	Thr	Tyr	His	Gln	Asn	Gln	Gly	Glu	Asn	Ile	Ser	Ser	245	250	255
Leu	Leu	Arg	Glu	Leu	Tyr	Ala	Lys	Pro	Leu	Ser	Glu	Arg	His	Val	Glu	260	265	270
Ser	Asp	Gly	Leu	Ile	Phe	Asp	Pro	Ala	Gln	Ile	Thr	Ser	Arg	Thr	Ala	275	280	285
Arg	Gly	Val	Ala	Val	Pro	His	Gly	Asn	His	Tyr	His	Phe	Ile	Pro	Tyr	290	295	300
Glu	Gln	Met	Ser	Glu	Leu	Glu	Lys	Arg	Ile	Ala	Arg	Ile	Ile	Pro	Leu	305	310	315
Arg	Tyr	Arg	Ser	Asn	His	Trp	Val	Pro	Asp	Ser	Arg	Pro	Glu	Glu	Pro	325	330	335
Ser	Pro	Gln	Pro	Thr	Pro	Glu	Pro	Ser	Pro	Ser	Pro	Gln	Pro	Ala	Pro	340	345	350
Ser	Asn	Pro	Ile	Asp	Glu	Lys	Leu	Val	Lys	Glu	Ala	Val	Arg	Lys	Val	355	360	365
Gly	Asp	Gly	Tyr	Val	Phe	Glu	Glu	Asn	Gly	Val	Ser	Arg	Tyr	Ile	Pro	370	375	380
Ala	Lys	Asp	Leu	Ser	Ala	Glu	Thr	Ala	Ala	Gly	Ile	Asp	Ser	Lys	Leu	385	390	395
Ala	Lys	Gln	Glu	Ser	Leu	Ser	His	Lys	Leu	Gly	Ala	Lys	Lys	Thr	Asp	405	410	415
Leu	Pro	Ser	Ser	Asp	Arg	Glu	Phe	Tyr	Asn	Lys	Ala	Tyr	Asp	Leu	Leu	420	425	430
Ala	Arg	Ile	His	Gln	Asp	Leu	Leu	Asp	Asn	Lys	Gly	Arg	Gln	Val	Asp	435	440	445
Phe	Glu	Ala	Leu	Asp	Asn	Leu	Leu	Glu	Arg	Leu	Lys	Asp	Val	Ser	Ser	450	455	460
Asp	Lys	Val	Lys	Leu	Val	Asp	Asp	Ile	Leu	Ala	Phe	Leu	Ala	Pro	Ile	465	470	475
Arg	His	Pro	Glu	Arg	Leu	Gly	Lys	Pro	Asn	Ala	Gln	Ile	Thr	Tyr	Thr	485	490	495
Asp	Asp	Glu	Ile	Gln	Val	Ala	Lys	Leu	Ala	Gly	Lys	Tyr	Thr	Thr	Glu	500	505	510
Asp	Gly	Tyr	Ile	Phe	Asp	Pro	Arg	Asp	Ile	Thr	Ser	Asp	Glu	Gly	Asp	515	520	525
Ala	Tyr	Val	Thr	Pro	His	Met	Thr	His	Ser	His	Trp	Ile	Lys	Lys	Asp	530	535	540
Ser	Leu	Ser	Glu	Ala	Glu	Arg	Ala	Ala	Ala	Gln	Ala	Tyr	Ala	Lys	Glu	545	550	555
Lys	Gly	Leu	Thr	Pro	Pro	Ser	Thr	Asp	His	Gln	Asp	Ser	Gly	Asn	Thr	565	570	575
Glu	Ala	Lys	Gly	Ala	Glu	Ala	Ile	Tyr	Asn	Arg	Val	Lys	Ala	Ala	Lys	580	585	590
Lys	Val	Pro	Leu	Asp	Arg	Met	Pro	Tyr	Asn	Leu	Gln	Tyr	Thr	Val	Glu	595	600	605
Val	Lys	Asn	Gly	Ser	Leu	Ile	Ile	Pro	His	Tyr	Asp	His	Tyr	His	Asn	610	615	620
Ile	Lys	Phe	Glu	Trp	Phe	Asp	Glu	Gly	Leu	Tyr	Glu	Ala	Pro	Lys	Gly	625	630	635
Tyr	Ser	Leu	Glu	Asp	Leu	Leu	Ala	Thr	Val	Lys	Tyr	Tyr	Val	Glu	His	645	650	655

Pro Asn Glu Arg Pro His Ser Asp Asn Gly Phe Gly Asn Ala Ser Asp
 660 665 670
 His Val Gln Arg Asn Lys Asn Gly Gln Ala Asp Thr Asn Gln Thr Glu
 675 680 685
 Lys Pro Asn Glu Glu Lys Pro Gln Thr Glu Lys Pro Glu Glu Glu Thr
 690 695 700
 Pro Arg Glu Glu Lys Pro Gln Ser Glu Lys Pro Glu Ser Pro Lys Pro
 705 710 715 720
 Thr Glu Glu Pro Glu Glu Glu Ser Pro Glu Glu Ser Pro Glu Glu Ser
 725 730 735
 Glu Glu Pro Gln Val Glu Thr Glu Lys Val Lys Glu Lys Leu Arg Glu
 740 745 750
 Ala Glu Asp Leu Leu Gly Lys Ile Gln Asn Pro Ile Ile Lys Ser Asn
 755 760 765
 Ala Lys Glu Thr Leu Thr Gly Leu Lys Asn Asn Leu Leu Phe Gly Thr
 770 775 780
 Gln Asp Asn Asn Thr Ile Met Ala Glu Ala Glu Lys Leu Leu Ala Leu
 785 790 795 800
 Leu Lys Glu Ser Lys
 805

<210> 101
 <211> 807
 <212> PRT
 <213> S. pneumoniae

<400> 101
 Cys Ser Tyr Glu Leu Gly Arg His Gln Ala Gly Gln Val Lys Lys Glu
 1 5 10 15
 Ser Asn Arg Val Ser Tyr Ile Asp Gly Asp Gln Ala Gly Gln Lys Ala
 20 25 30
 Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala
 35 40 45
 Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His
 50 55 60
 Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile
 65 70 75 80
 Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp
 85 90 95
 Ser Asp Ile Val Asn Glu Ile Lys Gly Gly Tyr Val Ile Lys Val Asp
 100 105 110
 Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Ile
 115 120 125
 Arg Thr Lys Glu Glu Ile Lys Arg Gln Lys Gln Glu Arg Ser His Asn
 130 135 140
 His Asn Ser Arg Ala Asp Asn Ala Val Ala Ala Ala Arg Ala Gln Gly
 145 150 155 160
 Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser Asp Ile Ile
 165 170 175
 Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asn His Phe His
 180 185 190
 Tyr Ile Pro Lys Ser Asp Leu Ser Ala Ser Glu Leu Ala Ala Ala Gln
 195 200 205
 Ala Tyr Trp Asn Gly Lys Gln Gly Ser Arg Pro Ser Ser Ser Ser
 210 215 220
 His Asn Ala Asn Pro Ala Gln Pro Arg Leu Ser Glu Asn His Asn Leu
 225 230 235 240

Thr	Val	Thr	Pro	Thr	Tyr	His	Gln	Asn	Gln	Gly	Glu	Asn	Ile	Ser	Ser	
				245					250					255		
Leu	Leu	Arg	Glu	Leu	Tyr	Ala	Lys	Pro	Leu	Ser	Glu	Arg	His	Val	Glu	
			260					265					270			
Ser	Asp	Gly	Leu	Ile	Phe	Asp	Pro	Ala	Gln	Ile	Thr	Ser	Arg	Thr	Ala	
		275					280					285				
Arg	Gly	Val	Ala	Val	Pro	His	Gly	Asn	His	Tyr	His	Phe	Ile	Pro	Tyr	
		290				295					300					
Ser	Gln	Met	Ser	Glu	Leu	Glu	Glu	Arg	Ile	Ala	Arg	Ile	Ile	Pro	Leu	
305					310					315					320	
Arg	Tyr	Arg	Ser	Asn	His	Trp	Val	Pro	Asp	Ser	Arg	Pro	Glu	Gln	Pro	
				325					330					335		
Ser	Pro	Gln	Ser	Thr	Pro	Glu	Pro	Ser	Pro	Ser	Pro	Gln	Ser	Ala	Pro	
			340					345					350			
Asn	Pro	Gln	Pro	Ala	Pro	Ser	Asn	Pro	Ile	Asp	Glu	Lys	Leu	Val	Lys	
		355					360					365				
Glu	Val	Val	Arg	Lys	Val	Gly	Asp	Gly	Tyr	Val	Phe	Glu	Lys	Asn	Gly	
		370				375					380					
Val	Ser	Arg	Tyr	Ile	Pro	Ala	Lys	Asn	Leu	Ser	Ala	Glu	Thr	Ala	Ala	
385					390					395					400	
Gly	Ile	Asp	Ser	Lys	Leu	Ala	Lys	Gln	Glu	Ser	Leu	Ser	His	Lys	Leu	
				405					410					415		
Gly	Ala	Lys	Lys	Thr	Asp	Leu	Pro	Ser	Ser	Asp	Arg	Glu	Phe	Tyr	Asn	
			420					425					430			
Lys	Ala	Tyr	Asp	Leu	Leu	Ala	Arg	Ile	His	Gln	Asp	Leu	Leu	Asp	Asn	
		435					440					445				
Lys	Gly	Arg	Gln	Val	Asp	Phe	Glu	Ala	Leu	Asp	Asn	Leu	Leu	Glu	Arg	
		450				455					460					
Leu	Glu	Asp	Val	Pro	Ser	Asp	Lys	Val	Lys	Leu	Val	Asp	Asp	Ile	Leu	
465					470					475					480	
Ala	Phe	Leu	Ala	Pro	Ile	Arg	His	Pro	Glu	Arg	Leu	Gly	Lys	Pro	Asn	
				485					490					495		
Ala	Gln	Ile	Thr	Tyr	Thr	Asp	Asp	Glu	Ile	Gln	Val	Ala	Lys	Leu	Ala	
			500					505					510			
Gly	Lys	Tyr	Thr	Thr	Glu	Asp	Gly	Tyr	Ile	Phe	Asp	Pro	Arg	Asp	Ile	
		515					520					525				
Thr	Ser	Asp	Glu	Gly	Asp	Ala	Tyr	Val	Thr	Pro	His	Met	Thr	His	Ser	
						535					540					
His	Trp	Ile	Lys	Lys	Asp	Ser	Leu	Ser	Glu	Ala	Glu	Arg	Ala	Ala	Ala	
545					550					555					560	
Gln	Ala	Tyr	Ala	Lys	Glu	Lys	Gly	Leu	Thr	Pro	Pro	Ser	Thr	Asp	His	
				565					570					575		
Gln	Asp	Ser	Gly	Asn	Thr	Glu	Ala	Lys	Gly	Ala	Glu	Ala	Ile	Tyr	Asn	
			580					585					590			
Arg	Val	Lys	Ala	Ala	Lys	Lys	Val	Pro	Leu	Asp	Arg	Met	Pro	Tyr	Asn	
		595					600					605				
Leu	Gln	Tyr	Thr	Val	Glu	Val	Lys	Asn	Gly	Ser	Leu	Ile	Ile	Pro	His	
		610				615					620					
Tyr	Asp	His	Tyr	His	Asn	Ile	Lys	Phe	Glu	Trp	Phe	Asp	Glu	Gly	Leu	
625					630					635					640	
Tyr	Glu	Ala	Pro	Lys	Gly	Tyr	Thr	Leu	Glu	Asp	Leu	Leu	Ala	Thr	Val	
				645					650					655		
Lys	Tyr	Tyr	Val	Glu	His	Pro	Asn	Glu	Arg	Pro	His	Ser	Asp	Asn	Gly	
			660					665					670			
Phe	Gly	Asn	Ala	Ser	Asp	His	Val	Gln	Arg	Asn	Lys	Asn	Gly	Gln	Ala	
		675					680					685				

Asp Thr Asn Gln Thr Glu Lys Pro Ser Glu Glu Lys Pro Gln Thr Glu
 690 695 700
 Lys Pro Glu Glu Glu Thr Pro Arg Glu Glu Lys Pro Gln Ser Glu Lys
 705 710 715 720
 Pro Glu Ser Pro Lys Pro Thr Glu Glu Pro Glu Glu Glu Ser Pro Glu
 725 730 735
 Glu Ser Glu Glu Pro Gln Val Glu Thr Glu Lys Val Glu Glu Lys Leu
 740 745 750
 Arg Glu Ala Glu Asp Leu Leu Gly Lys Ile Gln Asp Pro Ile Ile Lys
 755 760 765
 Ser Asn Ala Lys Glu Thr Leu Thr Gly Leu Lys Asn Asn Leu Leu Phe
 770 775 780
 Gly Thr Gln Asp Asn Asn Thr Ile Met Ala Glu Ala Glu Lys Leu Leu
 785 790 795 800
 Ala Leu Leu Lys Glu Ser Lys
 805

<210> 102
 <211> 821
 <212> PRT
 <213> S. pneumoniae

<400> 102
 Cys Ala Tyr Glu Leu Gly Leu His Gln Ala Gln Thr Val Lys Glu Asn
 1 5 10 15
 Asn Arg Val Ser Tyr Ile Asp Gly Lys Gln Ala Thr Gln Lys Thr Glu
 20 25 30
 Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile Asn Ala Glu
 35 40 45
 Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly
 50 55 60
 Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Ile Ile
 65 70 75 80
 Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp Ser
 85 90 95
 Asp Ile Val Asn Glu Ile Lys Gly Gly Tyr Val Ile Lys Val Asn Gly
 100 105 110
 Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg
 115 120 125
 Thr Lys Glu Glu Ile Asn Arg Gln Lys Gln Glu His Ser Gln His Arg
 130 135 140
 Glu Gly Gly Thr Ser Ala Asn Asp Gly Ala Val Ala Phe Ala Arg Ser
 145 150 155 160
 Gln Gly Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser Asp
 165 170 175
 Ile Ile Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asp His
 180 185 190
 Tyr His Tyr Ile Pro Lys Asn Glu Leu Ser Ala Ser Glu Leu Ala Ala
 195 200 205
 Ala Glu Ala Phe Leu Ser Gly Arg Glu Asn Leu Ser Asn Leu Arg Thr
 210 215 220
 Tyr Arg Arg Gln Asn Ser Asp Asn Thr Pro Arg Thr Asn Trp Val Pro
 225 230 235 240
 Ser Val Ser Asn Pro Gly Thr Thr Asn Thr Asn Thr Ser Asn Asn Ser
 245 250 255
 Asn Thr Asn Ser Gln Ala Ser Gln Ser Asn Asp Ile Asp Ser Leu Leu
 260 265 270

Lys Gln Leu Tyr Lys Leu Pro Leu Ser Gln Arg His Val Glu Ser Asp
 275 280 285
 Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr Ala Arg Gly
 290 295 300
 Val Ala Val Pro His Gly Asn His Tyr His Phe Ile Pro Tyr Glu Gln
 305 310 315 320
 Met Ser Glu Leu Glu Lys Arg Ile Ala Arg Ile Ile Pro Leu Arg Tyr
 325 330 335
 Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Glu Pro Ser Pro
 340 345 350
 Gln Pro Thr Pro Glu Pro Ser Pro Ser Pro Gln Pro Ala Pro Asn Pro
 355 360 365
 Gln Pro Ala Pro Ser Asn Pro Ile Asp Glu Lys Leu Val Lys Glu Ala
 370 375 380
 Val Arg Lys Val Gly Asp Gly Tyr Val Phe Glu Asn Gly Val Ser
 385 390 395 400
 Arg Tyr Ile Pro Ala Lys Asn Leu Ser Ala Glu Thr Ala Ala Gly Ile
 405 410 415
 Asp Ser Lys Leu Ala Lys Gln Glu Ser Leu Ser His Lys Leu Gly Ala
 420 425 430
 Lys Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu Phe Tyr Asn Lys Ala
 435 440 445
 Tyr Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp Asn Lys Gly
 450 455 460
 Arg Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu Arg Leu Lys
 465 470 475 480
 Asp Val Ser Ser Asp Lys Val Lys Leu Val Asp Asp Ile Leu Ala Phe
 485 490 495
 Leu Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro Asn Ala Gln
 500 505 510
 Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala Gly Lys
 515 520 525
 Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp Ile Thr Ser
 530 535 540
 Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His Ser His Trp
 545 550 555 560
 Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala
 565 570 575
 Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp
 580 585 590
 Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val
 595 600 605
 Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln
 610 615 620
 Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His Tyr Asp
 625 630 635 640
 His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu
 645 650 655
 Ala Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr
 660 665 670
 Tyr Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn Gly Phe Gly
 675 680 685
 Asn Ala Ser Asp His Val Gln Arg Asn Lys Asn Gly Gln Ala Asp Thr
 690 695 700
 Asn Gln Thr Glu Lys Pro Ser Glu Glu Lys Pro Gln Thr Glu Lys Pro
 705 710 715 720

Glu Glu Glu Thr Pro Arg Glu Glu Lys Pro Gln Ser Glu Lys Pro Glu
725 730 735
Ser Pro Lys Pro Thr Glu Glu Pro Glu Glu Glu Ser Pro Glu Glu Ser
740 745 750
Glu Glu Pro Gln Val Glu Thr Glu Lys Val Glu Glu Lys Leu Arg Glu
755 760 765
Ala Glu Asp Leu Leu Gly Lys Ile Gln Asp Pro Ile Ile Lys Ser Asn
770 775 780
Ala Lys Glu Thr Leu Thr Gly Leu Lys Asn Asn Leu Leu Phe Gly Thr
785 790 795 800
Gln Asp Asn Asn Thr Ile Met Ala Glu Ala Glu Lys Leu Leu Ala Leu
805 810 815
Leu Lys Glu Ser Lys
820

A1